RESEARCH ARTICLE

Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication [version 1; referees: 2 approved with reservations]

Ivan Nombela [1], Sara Puente-Marin[1], Verónica Chico[1], Alberto J. Villena[2], Begoña Carracedo[2], Sergio Ciordia[3], María Carmen Mena[3], Luis Mercado[4], Luis Perez [1], Julio Coll[5], Amparo Estepa[1+], Maria del Mar Ortega-Villaizan [1]

[1]Instituto de Biología Molecular y Celular, Universidad Miguel Hernández, Elche, Spain
[2]Área de Biología Celular, Departamento de Biología Molecular, Universidad de León, León, Spain
[3]Unidad de Proteómica, Centro Nacional de Biotecnología, Madrid, Spain
[4]Instituto de Biología, Pontificia Universidad Católica de Valparaíso, Valparaíso, Chile
[5]INIA-SIGT–Biotecnología, Madrid, Spain

[+] Deceased author

v1 **First published:** 06 Nov 2017, **6**:1958 (doi: 10.12688/f1000research.12985.1)
Latest published: 06 Nov 2017, **6**:1958 (doi: 10.12688/f1000research.12985.1)

Abstract

Background: It has been described that fish nucleated red blood cells (RBCs) generate a wide variety of immune-related gene transcripts when viruses highly replicate inside them and are their main target cell. The immune response and mechanisms of fish RBCs against viruses targeting other cells or tissues has not yet been explored and is the objective of our study.
Methods: Trout RBCs were obtained from peripheral blood, ficoll purified and exposed to *Viral Haemorrhagic Septicaemia virus* (VHSV). Immune response was evaluated by means of RT-qPCR, flow cytometry, immunofluorescence and isobaric tag for relative and absolute quantification (iTRAQ) protein profiling
Results: VHSV N gene transcripts incremented early postexposure and were drastically decreased after 6 hours postexposure (hpe). The expression of the type I interferon (*ifn1*) gene was significantly downregulated at early postexposure (3 hpe), together with a gradual downregulation of interferon-inducible *mx* and *pkr* genes until 72 hpe. Type I IFN protein was downregulated and interferon-inducible Mx protein was maintained at basal levels. Co-culture assays of RBCs with TSS (stromal cell line from spleen) revealed the IFN crosstalk between both cell types. On the other hand, anti-microbial peptide β-defensin 1 and neutrophil chemotactic factor interleukin 8 were slightly upregulated in VHSV-exposed RBCs Isobaric tag for relative and absolute quantification (iTRAQ) revealed that VHSV exposure can induce a global protein downregulation in trout RBCs, mainly related to RNA stability and proteasome pathways. The antioxidant/antiviral response is also suggested to be involved in the response of trout RBCs to VHSV.
Conclusions: A variety of mechanisms are proposed to be implicated in the antiviral response of trout RBCs against VHSV halted infection. Ongoing research is focused on understanding the mechanisms in detail. To our

Open Peer Review

Referee Status: ? ?

	Invited Referees 1	2
version 1 published 06 Nov 2017	? report	? report

1 **Aleksei Krasnov**, Nofima AS, Norway

2 **Johannes M. Dijkstra**, Fujita Health University, Japan

Discuss this article

Comments (0)

knowledge, this is the first report that implicates fish RBCs in the antiviral response against viruses not targeting RBCs.

Corresponding author: Maria del Mar Ortega-Villaizan (mortega-villaizan@umh.es)

Author roles: Nombela I: Formal Analysis, Investigation, Methodology, Validation, Writing – Review & Editing; **Puente-Marin S**: Formal Analysis, Investigation, Writing – Review & Editing; **Chico V**: Formal Analysis, Investigation, Methodology, Writing – Review & Editing; **Villena AJ**: Resources; **Carracedo B**: Resources; **Ciordia S**: Investigation, Methodology; **Mena MC**: Investigation, Methodology; **Mercado L**: Resources; **Perez L**: Writing – Review & Editing; **Coll J**: Writing – Review & Editing; **Estepa A**: Conceptualization; **Ortega-Villaizan MdM**: Conceptualization, Data Curation, Formal Analysis, Funding Acquisition, Investigation, Methodology, Project Administration, Resources, Supervision, Validation, Visualization, Writing – Original Draft Preparation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

How to cite this article: Nombela I, Puente-Marin S, Chico V *et al.* **Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication [version 1; referees: 2 approved with reservations]** *F1000Research* 2017, **6**:1958 (doi: 10.12688/f1000research.12985.1)

Grant information: This work was supported by the European Research Council (ERC starting grant 2014 GA639249).
The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

First published: 06 Nov 2017, **6**:1958 (doi: 10.12688/f1000research.12985.1)

Introduction

Fish are the most primitive vertebrates possessing many of the immune system cells (lymphocytes, NK cells, macrophages, etc) and molecules (interleukins, chemokins, receptors, etc) found in higher vertebrates. In contrast to higher vertebrates, however, fish lack bone marrow, lymph nodes, IgG-switch, and have tetrameric rather than pentameric IgM, with a more limited binding repertoire than mammals[1]. Furthermore, fish poikilothermic nature results in a delayed antigen affinity maturation, memory and lymphocyte proliferation[2]. To compensate for those immune deficiencies, fish have unique phagocytic B lymphocytes[3] and stronger innate immune responses, as shown in survivors of viral infection[4]. Furthermore, fish red blood cells (RBCs) have receptors capable of recognizing pathogen associated molecular patterns and respond to them with differentially expressed cytokine transcripts[5,6] and cytokine-like factors[7]. Thus, fish RBCs generate a wide variety of immune-related gene transcripts when viruses highly replicate inside them[8–10], while their mammalian counterparts are unable to do this. In light of this evidence, an outstanding question is whether fish RBCs are able to respond to viral infections that are well known to replicate in other cells or tissues, and if they could further contribute with compensatory immune responses in order to physiologically combat viral infections that do not target RBCs.

To explore *in vitro* the above mentioned question, we used rainbow trout *Oncorhynchus mykiss*), an important aquacultured species, together with the *Viral Haemorrhagic Septicemia virus* (VHSV), a rhabdovirus also called the 'fish ebola', which causes important losses of high economic impact on world-wide salmonid aquaculture[11]. VHSV viruses are bullet-shaped enveloped virions with single-stranded negative-sense RNA with a genome of 11.2 kbp[11–13]. VHSV do not target specifically RBCs, and therefore represent a good model to investigate the immune response of RBCs to viruses targeting other cells or tissues.

In this study, we describe how *in vitro* cultures of trout RBCs upregulated the expression of some immune proteins as part of their antiviral immune response against VHSV, whose infection appeared to be halted in trout RBCs. Simultaneously, the interferon-inducible *mx* and *pkr* genes showed a downregulation tendency during VHSV early replication, after 6 hours postexposure (hpe). In addition, the protein levels corresponding to BD1 (β-defensin 1 – an anti-microbial peptide known to be involved in antiviral innate immunity[14,15] and IL8 (Interleukin 8 – a neutrophil chemotactic factor), are shown, to our knowledge, for the first time, as characteristic of trout RBCs antiviral immune protein responses. Further, iTRAQ-based protein profiling of VHSV-exposed RBCs showed a global protein downregulation, mainly related to RNA stability and proteasome pathways. Related to this fact, the phosphorylation of the α-subunit of translational initiation factor 2 (eIF2α) and protein synthesis inhibition could be implicated in the inhibition of VHSV replication and RBCs proteome shut-off. Also, the antioxidant and related antiviral response is also suggested as involved in the response of trout RBCs to VHSV halted infection. In summary, we suggest a wide range of mechanisms implicated in the antiviral response of trout RBCs against VHSV halted infection

Methods

Animals

Rainbow trout (*Oncorhynchus mykiss*) individuals (number of individuals used are indicated in each assay) of approximately 5–6 cm were obtained from a VHSV-free commercial farm (PISZOLLA S.L., CIMBALLA FISH FARM, Zaragoza, Spain), and maintained at University Miguel Hernandez (UMH) facilities at 14°C, with a re-circulating dechlorinated-water system, at a stocking density of 1fish/3L, and fed daily with a commercial diet (SKRETTING, Burgos, Spain). Prior to experiments, fish were acclimatized to laboratory conditions over 2 weeks.

Antibodies

Rabbit polyclonal antibodies against rainbow trout β-defensin (BD1) (RRID: AB_2716268) (unpublished) and rainbow trout Mx3 (RRID: AB_2716267)[16,17] were produced at the laboratory of Dr. Amparo Estepa. Mouse polyclonal antibodies against rainbow trout IL1β (RRID: AB_2716269)[18,19] , IL8 (RRID: AB_2716272)[20], TNFα (RRID: AB_2716270)[21], Hepcidin (RRID: AB_2716273)[22], NKEF (RRID: AB_2716271)[23], IFN1 (RRID: AB_2716274) (unpublished) and IFNγ (RRID: AB_2716275) (unpublished) were produced at the laboratory of Dr. Luis Mercado. Rabbit polyclonal antibody against human NF-κβ p65 antibody (Cat#ab7970, RRID: AB_306184) was purchased from AbCam (Cambridge, UK). This p65 antibody epitope corresponds to the C-terminal region of the p65 protein, similarly to other p65 antibodies used for teleost species[24–26]. To label VHSV, we used the mouse monoclonal 2C9 antibody (RRID: AB_2716276)[27] against the N protein of VHSV (N_{VHSV}) produced at Dr. Coll's laboratory. Anti-Rabbit IgG (H+L) CF™ 488 antibody produced in goat and Anti-Mouse IgG (H+L) CF™ 488 antibody produced in goat were used as secondary antibodies (Sigma-Aldrich, Madrid, Spain). Rabbit polyclonal antibody against human eIF2α-P (Cat# E2152, RRID:AB_259283) and rabbit polyclonal antibody against human α-Actin (Cat#2066, RRID:AB_476693) were purchased from Sigma-Aldrich and used for western blotting.

Cell cultures and virus

Trout RBCs were obtained from peripheral blood of fish sacrificed by overexposure to tricaine (tricaine methanesulfonate, Sigma-Aldrich; 0.2 g/l). Peripheral blood was sampled from the caudal vein using insulin syringes (NIPRO, Bridgewater, NJ). Blood samples were placed in a 2 ml eppendorf with RPMI-1640 medium (Dutch modification) (Gibco, Thermo Fischer Scientific Inc., Carlsbad, CA) supplemented with 10% FBS (fetal bovine serum) gamma irradiated (Cultek, Madrid, Spain), 1 mM pyruvate (Gibco), 2 mM L-glutamine (Gibco), 50 µg/mL gentamicin (Gibco) and 2 µg/mL fungizone (Gibco), 100 U ml−1 penicillin and 100 µg ml−1 streptomycin (Sigma-Aldrich). Then, RBCs were purified by two consecutive density gradient centrifugations (7206g, Ficoll 1.007; Sigma-Aldrich). Purified RBCs were cultured in the above indicated medium at a density of $5{\cdot}10^5$ cells/ml in 24-well cell culture plates at 14°C and 5% CO_2.

The fish cell lines TSS, RTG-2 and EPC, were also used in this work. TSS (Trout Stroma from Spleen)[28] was donated by the laboratory of Dr. AJ Villena. TSS cells were maintained at 21°C in a 5% CO_2 atmosphere in RPMI-1640 medium containing 20% FBS,

1 mM pyruvate, 2 mM L-glutamine, 50 µg/mL gentamicin and 2 µg/mL fungizone. RTG-2 (Rainbow Trout Gonad-2) cell line was purchased from the American Type Culture Collection (ATCC, 50643). RTG-2 cells were maintained at 21°C in a 5% CO_2 atmosphere with MEM medium (Sigma-Aldrich) containing 10% FBS, 1 mM pyruvate, 2 mM L-glutamine, 50 µg/mL gentamicin and 2 µg/mL fungizone. EPC (*Epithelioma Papulosum Cyprini*)[29] cell line was purchased from the ATCC (CRL-2872). Cells were maintained at 28°C, in a 5% CO_2 atmosphere in RPMI-1640 10% FBS, 1 mM pyruvate, 2 mM L-glutamine, 50 µg/mL gentamicin and 2 µg/mL fungizone.

Viral haemorrhagic septicaemia virus (VHSV-07.71)[30], isolated in France from rainbow trout, *Oncorhynchus mykiss*, was purchased from the American Type Culture Collection (ATCC, VR-1388) and propagated in EPC cells at 14°C, as previously reported[31].

Viral exposure assays

RBCs and RTG-2 cells were infected with VHSV at different multiplicities of infection (MOI), at 14°C. After 3 hours of incubation for RBCs and 1.5 hours for RTG-2, cells were washed with cold RPMI, then RPMI 2% FBS was added and infection incubated at 14°C, at the different times indicated for each assay. In the case of the time-course assay, the virus was not removed.

Virus titers present in VHSV-exposed RBCs supernatants were determined by plaque assays. Briefly, different dilutions of the supernatants (from 10^{-1} to 10^{-4}) were added to EPC cell monolayers, grown in 24-well plates, at 14°C for 90 minutes. Then, the culture media were removed and infected cell monolayers covered with a solution of RPMI-1640 cell culture medium with 2% FBS and a 2% aqueous solution of methyl cellulose (Sigma-Aldrich). Cell plates were incubated at 14°C for 5 days and then the media with methyl cellulose was removed. Finally, EPC cell monolayers were stained with crystal violet-formalin to count plaques. Virus titers were expressed as plaque forming units (PFU) per ml.

Separately, N_{VHSV} RT-qPCR was also used to quantify the viral RNA inside VHSV-exposed RBCs (see below).

Blocking of endosome acidification by NH_4Cl

To block endosomal low-pH, NH_4Cl (Sigma-Aldrich) at 7 mM was added to RBCs during VHSV exposure, which was carried out as described in the previous section. No significant cell death was observed in RBCs treated with NH_4Cl, since the concentration used is known as non-cytotoxic, but effective for reducing VHSV infectivity by 40%[32]. After the incubation period, the viral titer in the supernatant was calculated as described in the previous section.

Neuraminidase treatment assay

Ficoll purified RBCs were pre-treated with 50 and 100 mU/ml of neuraminidase from *Vibrio cholerae* (Sigma-Aldrich), at 21°C for 30 minutes, before virus inoculation. After treatment, RBCs were washed once with PBS in order to completely remove the enzyme. After that, the pre-treated cells were inoculated with VHSV at MOI 1. RBCs inoculated with UV-inactivated VHSV were used as control. UV-inactivated VHSV was generated by exposure to UV-B at 1 J/cm2 using a Bio-Link Crosslinker BLX E312 (Vilber Lourmat, BLX-E312), as previously described[33]. The infection was monitored by RT-qPCR of the N_{VHSV} gene 3 at 72 hpe.

Co-culture assay

One day prior to the co-culture, RBCs, extracted and seeded as indicated before, were stimulated using UV-inactivated VHSV over 24 hours. Subsequently, RBCs were washed once with cold RPMI and added to Corning® Transwell® polyester membrane cell culture inserts of 0.4 µm pore size (Corning, Sigma-Aldrich) on 24 well plates with previously cultured confluent TSS cells in RPMI 20% FBS. Co-culture was maintained for 24 hours at 14°C in RPMI 2% FBS. After that, cells were washed and stored in the indicated buffer and conditions for RNA extraction.

RNA isolation and cDNA synthesis

E.Z.N.A. ® Total RNA Kit (Omega Bio-Tek, Inc., Norcross, GA) was used for total RNA extraction in accordance with the manufacturer's instructions. Isolated RNAs were stored at −80 °C until used. DNAse treatment was done in order to eliminate residual genomic DNA using TURBO™ DNase (Ambion, Thermo Fischer Scientific Inc.), following the manufacturer's instructions. RNA was quantified with a NanoDrop® Spectrophotometer (Nanodrop Technologies, Wilmington, DE). M-MLV reverse transcriptase (Invitrogen, Thermo Fischer Scientific Inc.) was used to obtain cDNA, as previously described[34].

RT-qPCR and gene expression

Real-Time Quantitative PCR (RT-qPCR) was performed using the ABI PRISM 7300 System (Applied Biosystems, Thermo Fischer Scientific Inc.). Reactions were performed in a total volume of 20 µl comprising 12 ng of cDNA, 900 nM of each primer, 10 µl of TaqMan universal PCR master mix (Applied Biosystems, Thermo Fischer Scientific Inc.) with 300 nM of probe or 10 µl of SYBR green PCR master mix (Applied Biosystems, Thermo Fischer Scientific Inc.). The cycling conditions were 50°C for 2 min and 95°C for 10 min, followed by 40 cycles at 95°C for 15 s and 60°C for 1 min. Primers and probes used are listed in Table 1.

Gene expression was analyzed by the 2-ΔCt or 2−ΔΔCt method[35] where 18S rRNA or *ef1α* gene (Applied Biosystems, Thermo Fischer Scientific Inc.) were used as endogenous control.

Intracellular stain and flow cytometry

RBCs were fixed with 4% paraformaldehyde (PFA; Sigma-Aldrich) in RPMI 1640 medium for 20 minutes. Permeabilization of the RBCs was done in a 0.05% saponin (Sigma-Aldrich) buffer for 15 minutes. Primary antibodies were diluted in the permeabilization buffer at the recommended dilutions and incubated for 60 minutes at RT. Secondary antibodies were incubated for 30 minutes at RT. After every antibody incubation, RBCs were washed with the permeabilization buffer. Finally, RBCs were kept in PFA 1% in PBS. For nuclear staining, RBCs were stained with 1 µg/mL of 4′-6-Diamidino-2-phenylindole (DAPI; Sigma-Aldrich) for 5 minutes. RBCs were analyzed by flow cytometry (FC) in a BD FACSCanto™ (BD Biosciences) flow cytometer. Immunofluorescence (IF) images were performed in an IN Cell Analyzer 6000 Cell Imaging system (GE Healthcare, Little Chalfont, UK).

Table 1. Primer and probe sequences.

Gene	Forward primer (5' – 3')	Reverse primer (5' – 3')	Probe (5' – 3')	Reference or accession number
ef1α	ACCCTCCTCTTGGTCGTTTC	TGATGACACCAACAGCAACA	GCTGTGCGTGACATGAGGCA	91
tlr3	ACTCGGTGGTGCTGGTCTTC	GAGGAGGCAATTTGGACGAA	CAAGTTGTCCCGCTGTCTGCTCCTG	NM_001124578.1
irf7	CCCAGGGTTCAGCTCCACTA	GGTCTGGCAACCCGTCAGT	TCGAGCCAAACACCAGCCCCT	AJ829673
ifn1	ACCAGATGGGAGGAGATATCACA	GTCCTCAAACTCAGCATCATCTATGT	AATGCCCCAGTCCTTTTCCCAAATC	AM489418.1
mx1-3	TGAAGCCCAGGATGAAATGG	TGGCAGGTCGATGAGTGTGA	ACCTCATCAGCCTAGAGATTGGCTCCCC	92
pkr	GACACCGCGTACCGATGTG	GGACGAACTGCTGCCTGAAT	CACCACCTCTGAGAGCGACACCACTTC	NM_001145891.1
hepcidin	TCCCGGAGCATTTCAGGTT	GCCCTTGTTGTGACAGCAGTT	AGCCACCTCTCCCTGTGCCGTTG	AF281354.1
β-globin	CAACATCTTGGCCACATACAAGTC	TTGTCAGGGTCGACGAAGAGT		NM_001160555.2
fth	GGCGTATTACTTCGATCGTGATG	CCCTCCCCTCTGGTTCTGA		EU302524.1
gstp1	CCCCTCCCTGAAGAGTTTTGT	GCAGTTTCTTGTAGGCGTCAGA		BT048561.1
nkef	CGCTGGACTTCACCTTTGTGT	ACCTCACAACCGATCTTCCTAAAC		U27125.1
sod1	GCCGGACCCCACTTCAAC	CATTGTCAGCTCCTGCAGTCA		AF469663.1
trx	AGACTTCACAGCCTCCTGGT	ACGTCCACCTTGAGGAAAAC		XM_021614924.1
N_{VHSV}	GACTCAACGGGACAGGAATGA	GGGCAATGCCCAAGTTGTT	TGGGTTGTTCACCCAGGCCGC	34

F1000Research 2017, 6:1958 Last updated: 30 NOV 2017

Protein digestion and tagging with iTRAQ 4plex™ reagent

Two pools of eight samples (two control: C1 and C2, and two VHSV-exposed: V1 and V2), with $8{\cdot}10^6$ cells per sample, were used for iTRAQ 4plex protein profiling.

The pools, containing $6.4{\cdot}10^7$ cells, were pelletized by centrifugation (5 min, 700 × g). The supernatant was carefully removed and the RBC pellets (~70–100 µL) were mixed with 250 µL of deionized water and frozen at – 80°C for 3 h. After thawing the lysate, it was centrifuged at 17000 × g for 20 min at 4°C to separate the cytosolic supernatant and the pelleted membrane fractions, as described in Nombela *et al*. (unpublished report, Nombela I, Ciordia S, Mena MC, Puente-Marin S, Chico V, Coll J, and Ortega-Villaizan M). Subsequently, a new proteomic analysis method was carried out that combines fractionation into cytosolic and membrane fractions, haemoglobin removal of the cytosolic fraction, protein digestion, pH reversed-phase peptide fractionation and finally LC ESI-MS/MS analysis of each of the fractions, as described in Nombela *et al*. (unpublished report, as before). Briefly, the haemoglobin of the cytosolic fraction was removed using a column of HemoVoid™ kit (Biotech Support Group, Monmouth Junction, NJ), following the manufacturer instructions[36]. For protein digestion of each fraction, 120 µg from haemoglobin-depleted cytosolic fraction were digested in the chaotropic buffer, and 40 µg of membrane fraction was precipitated by methanol/chloroform method and re-suspended in 20 µl of the chaotropic buffer. The digested samples (membrane and cytosol separately) were subsequently labelled using iTRAQ-4plex Isobaric Mass Tagging Kit (SCIEX), according to the manufacturer's instructions as follows: 114, C1 (Pool control 1); 115, V1 (Pool VHSV-exposed 1); 116, C2 (Pool control 2); 117, V2 (Pool VHSV-exposed 2). Then, offline high pH reversed-phase peptide fractionation of the peptides from the cytosolic RBC fraction was performed on a SmartLine (Knauer, Berlin, Germany) HPLC system using an XBridge C18 column (100 × 2.1 mm, 5 µm particle; Waters, Milford, MA). Thirty fractions were collected and then pooled alternatively into 5 fractions. After labelling, the samples were pooled, evaporated to dryness and stored at -20°C until LC−MS analysis.

Liquid chromatography and mass spectrometry analysis (LC-MS)

A 1 µg aliquot of labelled mixture was subjected to 1D-nano LC ESI-MSMS (Liquid Chromatography Electrospray Ionization Tandem Mass Spectrometric) analysis using a nano liquid chromatography system (Eksigent Technologies nanoLC Ultra 1D plus, SCIEX,) coupled to high speed Triple TOF 5600 mass spectrometer (SCIEX) with a Nanospray III source. The analytical column used was a silica-based reversed phase Acquity UPLC® M-Class Peptide BEH C18 Column, 75 µm × 150 mm, 1.7 µm particle size and 130 Å pore size (Waters Corporation, Milford, MA). The trap column was a C18 Acclaim PepMap™ 100 (Thermo Fischer Scientific), 100 µm × 2 cm, 5 µm particle diameter, 100 Å pore size, switched on-line with the analytical column. The loading pump delivered a solution of 0.1% formic acid in water at 2 µl/min. The nano-pump provided a flow-rate of 250 nl/min and was operated under gradient elution conditions. Peptides were separated using a 250 minutes gradient ranging from 2% to 90% mobile phase B (mobile phase A: 2% acetonitrile, 0.1% formic acid; mobile phase B: 100% acetonitrile, 0.1% formic acid). Injection volume was 5 µl.

Data acquisition was performed with a TripleTOF 5600 System (SCIEX). Data was acquired using an ionspray voltage floating, 2300 V; curtain gas, 35; interface heater temperature, 150; ion source gas 1, 25; declustering potential, 150 V. All data was acquired using information-dependent acquisition (IDA) mode with Analyst TF 1.7 software (RRID: SCR_015785) (SCIEX). For IDA parameters, 0.25 s MS survey scan in the mass range of 350–1250 Da were followed by 30 MS/MS scans of 150ms in the mass range of 100–1800. Switching criteria were set to ions greater than mass to charge ratio (m/z) 350 and smaller than m/z 1250 with charge state of 2–5 and an abundance threshold of more than 90 counts (cps). Former target ions were excluded for 20 s. IDA rolling collision energy (CE) parameters script was used for automatically controlling the CE.

Proteomics data analysis and sequence search

MS/MS spectra were exported to MGF format using Peak View v1.2.0.3 (RRID: SCR_015786)(SCIEX) and searched using Mascot Server v2.5.1 (RRID:SCR_014322)(Matrix Science, London, UK), OMSSA v2.1.9[37], X!TANDEM 2013.02.01.1[38], and Myrimatch v2.2.140[39] against a composite target/decoy database built from the Oncorhynchus mykiss sequences at Uniprot/Swissprot Knowledgebase (available here, last update: 2017/01/26, 50.125 sequences), together with commonly occurring contaminants. Search engines were configured to match potential peptide candidates with mass error tolerance of 25 ppm and fragment ion tolerance of 0.02D, allowing for up to two missed tryptic cleavage sites and a maximum isotope error (^{13}C) of 1, considering fixed methyl methanethiosulfonate modification of cysteine and variable oxidation of methionine, pyroglutamic acid from glutamine or glutamic acid at the peptide N-terminus, acetylation of the protein N-terminus, and modification of lysine, tyrosine and peptide N-terminus with iTRAQ 4-plex reagents. Score distribution models were used to compute peptide-spectrum match *P*-values[40], and spectra recovered by a FDR (False Discovery Rate) ≤ 0.01 (peptide-level) filter were selected for quantitative analysis. Approximately 1% of the signals with the lowest quality were removed prior to further analysis. Differential regulation was measured using linear models[41], and statistical significance was measured using *q*-values (FDR). All analyses were conducted using Proteobotics software (Isobaric Tagging Analysis Workflow v.1.0, RRID:SCR_015787; Madrid, Spain). The cutoff for differentially regulated proteins was established at FDR *q*-value 5%.

Pathway enrichment analysis

In order to evaluate the functionally grouped Gene Ontology (GO) and pathway annotation networks of the differentially expressed proteins, pathway enrichment analysis was performed using ClueGO (RRID:SCR_005748)[42] and CluePedia (RRID: SCR_015784)[43] Cytoscape plugins (Cytoscape v3.4.0, RRID: SCR_003032,[44]). GO Biological process, GO Immunological process, KEGG (Kyoto Encyclopedia of Genes and Genomes), Wikipathways and Reactome functional pathway databases were

used. A *P*-value ≤0.05 and Kappa score of 0.4 were considered as threshold values.

Western blot assays

Control and VHSV-exposed RBCs cell pellets were resuspended in 30 µl of PBS with a cocktail of protease inhibitors (Sigma-Aldrich). Cells were then frozen/thawed 3 times and protein concentration adjusted before loading. Samples were loaded in Tris–Glycine sodium dodecyl sulfate 17% polyacrylamide gels under reducing conditions. Electrophoresis was performed at 100 V for 90 min. For blotting, the proteins in the gel were transferred for 75 min at 100 V in transfer buffer (2.5 mM Tris, 9 mM glycine, 20% methanol) to nitrocellulose membranes (BioRad, Madrid, Spain). The membranes were then blocked with 8% dry milk, 1% Tween-20 in PBS and incubated with rabbit polyclonal antibody against human eIF2α-P (36.1 KDa) or rabbit polyclonal antibody against human α-Actin (42 KDa,) in PBS containing 0.5% dry milk, and 0.5% Tween-20 (PMT buffer), overnight at 4°C. Membranes were then washed 3 times with PMT buffer for 15 min before incubation with GAR-Po (Sigma-Aldrich) in PMT buffer for 45 min. Finally, the membrane was washed 3 times with PBS containing 0.5% Tween-20. Peroxidase activity was detected using ECL chemiluminescence reagents (Amersham Biosciences, Buckinghamshire, UK) and revealed by exposure to X-ray. Protein bands were analyzed by densitometry using the Scion Image 4.0.2 Software (RRID: SCR_008673) (www.scionorg.com).

ROS measurement

The intracellular ROS level was assessed in VHSV-exposed RBCs using the cell-permeant 2',7'-dichlorodihydrofluorescein diacetate (DCFDA, Sigma-Aldrich). RBCs were exposed to VHSV at MOI 1, during 72 h, at 14°C. After that, RBCs were washed with I and incubated with 20 µM DCFDA in RPMI, for 30 min at RT. The fluorescence intensity of 2′,7′-dichlorofluorescin was measured using the POLARstar Omega microplate reader (BMG LABTECH, USA) at excitation 480 nm and emission 530 nm.

Software and statistics

Graphpad Prism 6 (RRID:SCR_002798, www.graphpad.com) was used for graphic representation and statistics calculation. The statistic tests and *P*-values associated with the graphics are indicated in each assay. Flow cytometry data was processed and analyzed using *Flowing Software 2.5.1* (www.flowingsoftware.com/) (RRID: SCR_015781).

Ethics statement

All experimental protocols and methods of the experimental animals were reviewed and approved by the Animal Welfare Body and the Research Ethics Committee at the University Miguel Hernandez (approval number 2014.205.E.OEP; 2016.221.E.OEP) and by the competent authority of the Regional Ministry of Presidency and Agriculture, Fisheries, Food and Water supply (approval number 2014/VSC/PEA/00205). All methods were carried out in accordance with the Spanish Royal Decree RD 53/2013 and EU Directive 2010/63/EU for the protection of animals used for research experimentation and other scientific purposes.

Results

VHSV course of replication in trout RBCs

For this analysis we first purified RBCs (oval nucleated cells) to 99.9% (as evaluated by optical microscopy) and then exposed the purified RBCs to VHSV, for different times, to monitor the replication of VHSV in trout RBCs. For that, time course expression of the N gene of VHSV (N_{VHSV}) was measured by RT-qPCR. Clearly, the expressions of N_{VHSV} gene were significantly upregulated at 3 hours postexposure (hpe). However, they drastically decreased from 6 to 72 hpe, indicating that VHSV could replicate at early times postexposure, at the same levels as the VHSV susceptible trout cell line RTG-2. However, viral replication was halted in RBCs at later stages of infection, in contrast to RTG-2 (Figure 1A). On the other hand, after VHSV enters the cell, the first gene that starts to transcribe is the N_{VHSV} gene, since it is the closest to the 3' transcriptional start, and the more distal, excluding the polymerase, is the G glycoprotein gene (G_{VHSV}) gene. Therefore, under a normal transcription scenario a high ratio between the N_{VHSV} and G_{VHSV} viral genes transcripts is to be expected, taking into account the attenuation phenomenon found in rhabdoviruses[45]. However, a ratio of 2 was observed in RBCs, compared to the ratio of 8 found in RTG-2 cells, at 1 and 3 hpe (Figure 1B).

Also, RBCs were exposed to different VHSV multiplicities of infection (MOI). The initial VHSV inoculum titer declined ~3-logs after 3 days of incubation at the indicated MOI assayed (1, 10 or 100, respectively corresponding to inoculum virus titers $2{\cdot}10^6$, $2{\cdot}10^7$, $2{\cdot}10^8$ PFU/ml) (Figure 1C), in contrast to the usual 1-log titer increment in RTG-2 cells infected in the same conditions (Figure 1H). Later on, RBCs showed only a minor ~1-fold increment of the VHSV titer as the time of infection increased from 3 to 6 days (Figure 1D). These low VHSV titers were due to true VHSV internalization and not to residual VHSV binding, since they were NH_4Cl-sensitive, a characteristic of rhabdovirus infections (Figure 1D). NH_4Cl acts as a lysosomotropic drug, blocking endosomal acidification and inhibiting rhabdoviral cytoplasmic entrance steps including those of VHSV[46]. N_{VHSV} RT-qPCR also confirmed the presence of viral RNA in VHSV-exposed RBCs (Figure 1C).

In order to increase the amount of VHSV inside trout RBCs, RBCs were pre-treated with neuraminidase (NA) and then exposed to VHSV. NA has been shown to enhance rhabdovirus infection in NA pre-treated cells by favoring interaction with cellular membranes[47]. As a result, the VHSV RNA inside RBCs was increased about ten times at 3 hpe. However, seventy-two hpe the VHSV RNA drastically decreased to almost disappear, as indicated by N_{VHSV} RT-qPCR (Figure 1E).

Besides, N_{VHSV} protein (2C9 antibody) was detected in RBCs exposed to VHSV MOI 100, at 24 hpe, but not at 72 hpe. IF images (Figure 1F) showed an intracellular stain along the cytoplasm and nucleus. FC histogram (Figure 1G) showed a slight increment of VHSV N protein in VHSV-exposed RBCs, at 24 hpe, but not at 72 hpe. VHSV could not be detected by IF or FC in RBCs exposed to lower MOIs. Strikingly, N_{VHSV} protein stain was located mainly in the nuclear region of VHSV-exposed RBCs. Although it has

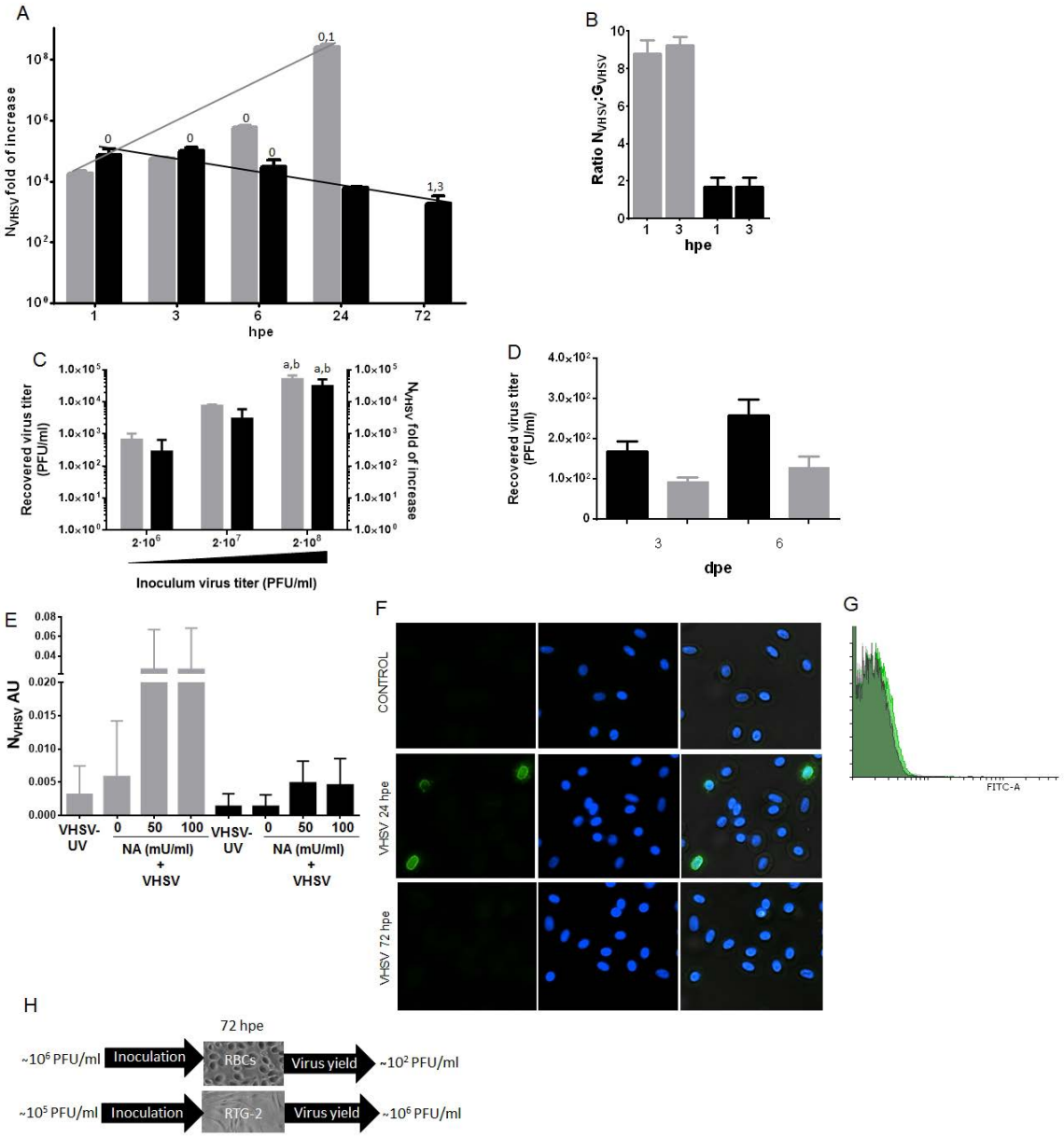

Figure 1. VHSV exposure and replication in trout RBCs. (**A**) Time course of VHSV gene replication in trout RBCs and RTG-2 cell line. N gene of VHSV (N_{VHSV}) expression profile was quantified at time 0, 1, 3, 6, 24 and 72 hours postexposure (hpe) to VHSV, in RBCs (black bars) and RTG-2 (grey bars), with a multiplicity of infection (MOI) of 1 at 14°C. Gene expression was normalized against eukaryotic 18S rRNA and *ef1α*, respectively for RBCs and RTG-2 cells, and relativized to control cells (time 0) (fold of increase). Data represent the mean ± SD (n = 4 for RBCs and n=2 for RTG-2). (**B**) Ratio of N_{VHSV} and G_{VHSV} genes (N_{VHSV}:G_{VHSV}) viral genes at time 0, 1, and 3 hpe in RBCs (black bars) and RTG-2 (grey bars). Gene expression was normalized against *ef1α*. Data represent the mean ± SD (n = 3 for RBCs and n=2 for RTG-2). (**C**) Viral yield in VHSV-exposed trout RBCs. Viral titer (grey bars) (plaque forming units per millilitre, PFU/ml) and N_{VHSV} gene expression (black bars) of VHSV-exposed RBCs, with MOI 1, 10 and 100, respectively corresponding to inoculum virus titers $2{\cdot}10^6$ (**a**), $2{\cdot}10^7$ (**b**) and $2{\cdot}10^8$ (**c**) PFU/ml, 72 hpe, at 14°C. Gene expression was normalized against *ef1α*. Data represent the mean ± SD (n = 3 for viral titer and n=4 for N_{VHSV} gene expression). (**D**) VHSV internalization in trout RBCs is NH_4Cl-sensitive. VHSV titers obtained in VHSV-exposed RBCs at MOI 1, at 3 and 6 days postexposure (dpe), at 14°C, in the absence (black bars) or in the presence (grey bars) of NH_4Cl. Data represent the mean ± SD (n = 4). (**E**) Pre-treatment of RBCs with neuraminidase enhances early replication of VHSV. RBCs were inoculated with UV-inactivated or live VHSV, with a MOI of 1, at 14°C. Before infection, cells were pretreated with neuraminidase (NA) at 50 or 100 mU/ml during 30 minutes at 14°C. VHSV infectivity was quantified by N_{VHSV} gene expression analysis at 3 hpe (grey bars) and 72 hpe (black bars). Gene expression was normalized against 18S rRNA gene and represented as arbitrary units (AU). Data represent the mean ± SD (n = 4). (**F**) Representative immunofluorescence of VHSV labelling in RBCs exposed to VHSV (MOI 100, 24 and 72 hpe, 14°C) stained from left to right with anti-N_{VHSV} 2C9 (FITC), DAPI for nuclei stained and merged (IF representative of 32 images). (**G**) Representative flow cytometry overlay histograms showing untreated RBCs (grey filled histogram), VHSV-exposed RBCs with a MOI 100, at 14°C, 24 hpe (green filled histogram) and 72 hpe (black filled histogram). (**H**) Schematic representation of the VHSV infectivity in RBCs and RTG-2 cells, indicating the virus inoculation titer and recovered virus yield after 72 hpe in each cell line. Kruskal-Wallis Test with Dunn´s Multiple Comparison post-hoc test was performed for statistical analysis among all conditions. Values over the bars denote pairwise significant differences with the value-indicated time point or condition (*P*-value < 0.05).

not been described that N_{VHSV} protein can be localized in the cell nucleus, another rhabdovirus proteins, such as rabies virus P3 protein[48] and the IHNV NV protein[49] have been localized in the nucleus of infected cells.

Antiviral transcriptional immune responses in trout RBCs exposed to VHSV *in vitro*

We next investigated whether trout RBCs exposed to VHSV could be capable of generating immune responses *in vitro*, by means of examining the differential expression profile of some genes characteristic of the fish antiviral response. First, a time course monitoring of the expression of the interferon-inducible *mx* and *pkr* genes was carried out at different time postexposure. The results showed that the *mx* and *pkr* genes exhibited the same increment peak at 3 hpe and the tendency to downregulation from 6 to 72 hpe, in parallel to N_{VHSV} gene transcription levels tendency (Figure 2A and B, and Figure 1A). On the other hand, at 3 hpe, *ifn1* gene expression already exhibited a statistically significant downregulation (Figure 2C), and a slight downregulation for *tlr3* and *irf7* genes.

Antiviral immune protein responses in RBCs exposed to VHSV *in vitro*

The changes in the RBCs immune protein response induced by VHSV exposure were assessed using specific antibodies. VHSV-exposed RBCs showed only an increment in individual protein levels of chemokine IL8 (Figure 3B and E, Figure S1) and antimicrobial peptide BD1 (Figure 3C and F, Figure S1), verified by means of FC and IF. Mx and IFN1 protein levels, according to the RT-qPCR results, did not change or downregulate, respectively (Figure 3A). Cytokines IL1β, IFNγ (Figure 3B), the antimicrobial peptide Hepcidin (Figure 3C) and the natural killer enhancing factor (NKEF) (Figure 3D) did not show regulation at 72 hpe.

It is noteworthy to highlight the elevated inter-individual variability found in trout RBCs immune response, for most of the proteins

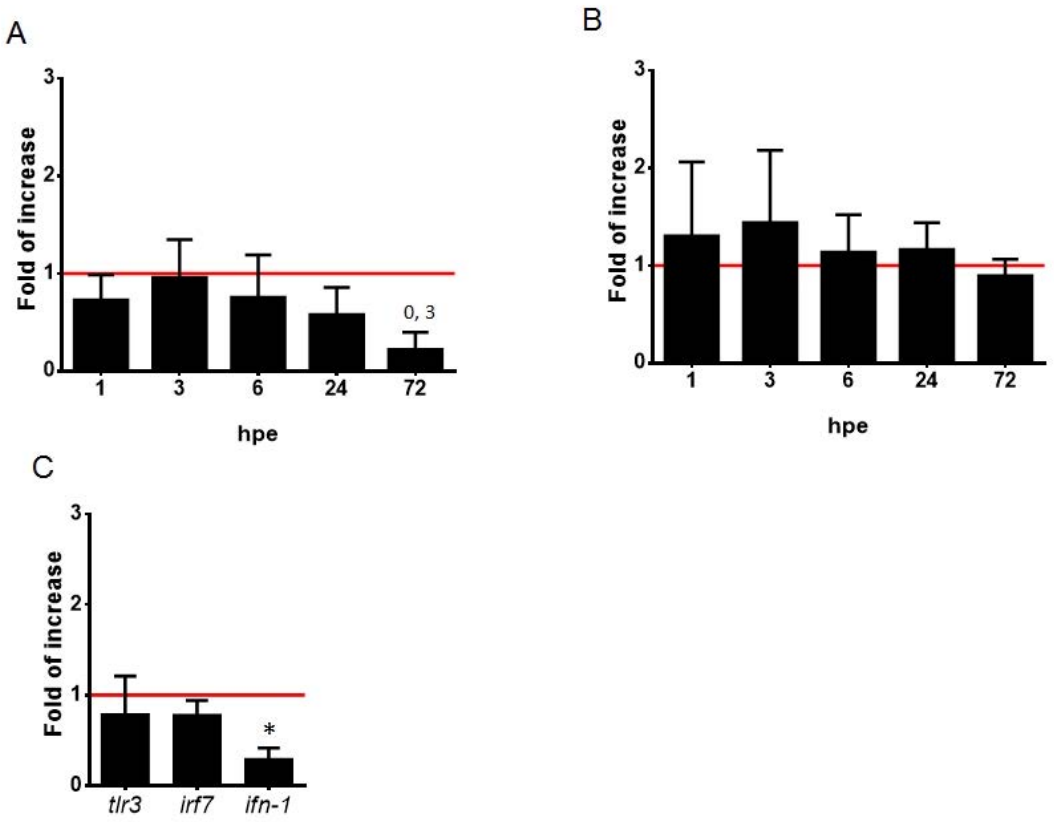

Figure 2. Interferon signaling in VHSV-exposed trout RBCs. Time course of interferon-inducible antiviral genes *mx* (**A**) and *pkr* (**B**). RBCs were exposed to VHSV with a multiplicity of infection (MOI) of 1 at 14°C, and *mx1-3* and *pkr* genes expression was quantified at time 0, 1, 3, 6, 12, 24, 72 hours postexposure (hpe). Data is displayed as mean ± SD (n = 3). Kruskal-Wallis Test with Dunn´s Multiple Comparison post-hoc test was performed among all conditions. (**C**) Interferon signaling at early time postexposure. RBCs were exposed to VHSV with a MOI of 1 at 14°C, and *tlr3*, *irf7* and *ifn1* gene expression profiles were quantified at time 0, and 3 hpe. Data is displayed mean ± SD (n = 3). Mann Whitney Test was performed for statistical analysis between the VHSV-exposed and control cells. Gene expression was normalized against eukaryotic 18S rRNA for *mx, tlr3, irf7* and *ifn1* genes and *ef1α* for *pkr* gene, and relativized to control cells (time 0, red line) (fold of increase). Asterisk denote statistically significant differences between the VHSV-exposed and the control cells (*P*-value < 0.05).

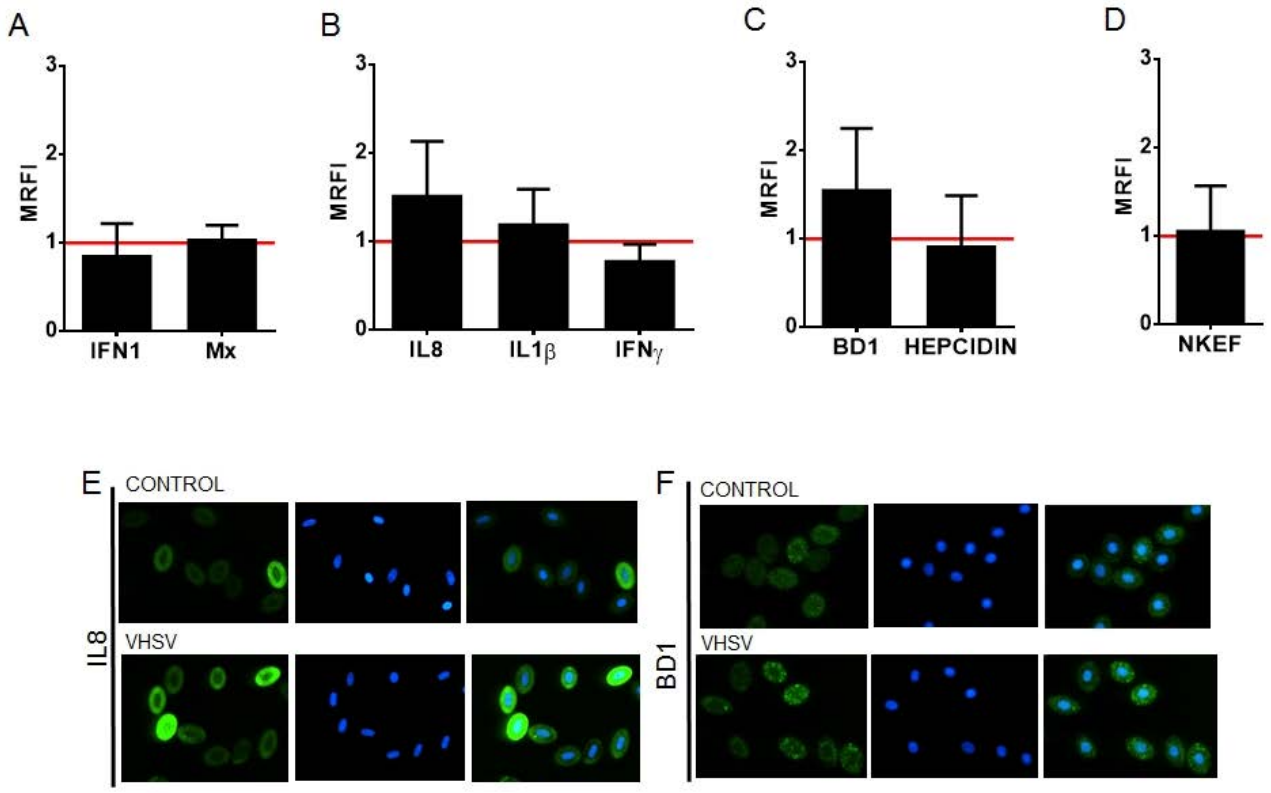

Figure 3. Immune protein responses of VHSV-exposed RBCs. Relative immune protein expression levels, (**A**) interferon pathway related proteins (IFN1 and Mx), (**B**) antimicrobial peptides (BD1 and Hepcidin), (**C**) cytokines (IL8, IL1β and IFNγ) and (**D**) antioxidant protein NKEF, measured by flow cytometry and calculated by the formula MRFI (Mean Relative Fluorescence Intensity) = fluorescence in VHSV-exposed RBCs / fluorescence in non-exposed RBCs, at multiplicity of infection (MOI) 1, 72 hours postexposure (hpe), at 14°C, relative to control cells (red line). Data is displayed as mean ± SD (n=5). Mann Whitney Test was performed for statistical analysis between the VHSV-exposed cells and control cells. Representative immunofluorescences of control and VHSV-exposed RBCs stained with anti-IL8 (IF representative of 44 images) (**E**) and anti-BD1 (IF representative of 46 images) (**F**) (FITC) and DAPI for nuclei stain.

and genes assayed, which could prevent to obtain statistical significance in most of the cases although regulations were apparent.

Interferon crosstalk between RBCs and the spleen stromal TSS cell line

The rainbow trout spleen is an active hematopoietic organ[50], and it is composed of various cell types, such as red blood cells, leukocytes and reticular or stromal cells[51]. It has been demonstrated that cytokines and soluble factors produced by the stromal cells are required for trout blood cells development in the spleen or head kidney[52]. In this regard, we wanted to evaluate the paracrine effects of the cytokines produced by VHSV stimulated RBCs over the stromal cell line from trout spleen, TSS[28]. For that, trout RBCs stimulated with VHSV UV-inactivated were co-culture with the TSS cell line, using a Transwell system to test whether a cross-stimulation mediated by soluble molecules was involved. The gene expression profiles for *ifn1*, and the interferon stimulated genes (ISGs) *mx*, viral inducible gene *vig1*, and interleukin *il15* genes were examined for each cell line 24 hours post co-culture. Linear regression analysis of the RBCs *ifn1* gene expression with their respective *mx*, *vig1* and *il15* genes showed a significant correlation between *ifn1* and *vig1* and *il15*, but not with *mx* gene (Figure 4A). *ifn1* gene expression from RBCs and TSS cells also showed a significant correlation (Figure 4B). TSS cells showed significant correlation between *ifn1* and *mx*, *vig1* and *il15* (Figure 4C). The results demonstrated an IFN crosstalk between the stimulated RBCs and TSS cells.

iTRAQ protein profile of VHSV-exposed RBCs

The iTRAQ data showed a total of 9246 MS/MS Spectra, 2639 unique peptides with peptide-level FDR<0.01 and 872 inferred proteins common in all samples. Significant up/down regulations between samples were determined by a log2FoldChange)>1 with a *q*-value<0.05. In total, 64 proteins were significantly up or down-regulated during VHSV exposure (Figure 5). Specifically, 59 proteins were downregulated and only 5 proteins were upregulated during VHSV exposure. Cytoscape functional annotation was used to investigate the underlying biologically functional differences that may be related to VHSV exposure. The results showed four strongly represented networks of interest (mRNA stability, proteasome, viral process and cellular catabolic processes) (Figure 5 and Figure S2). Among the 59 down-regulated proteins (Figure 6, Table S1), the top-score network was the mRNA stability, being

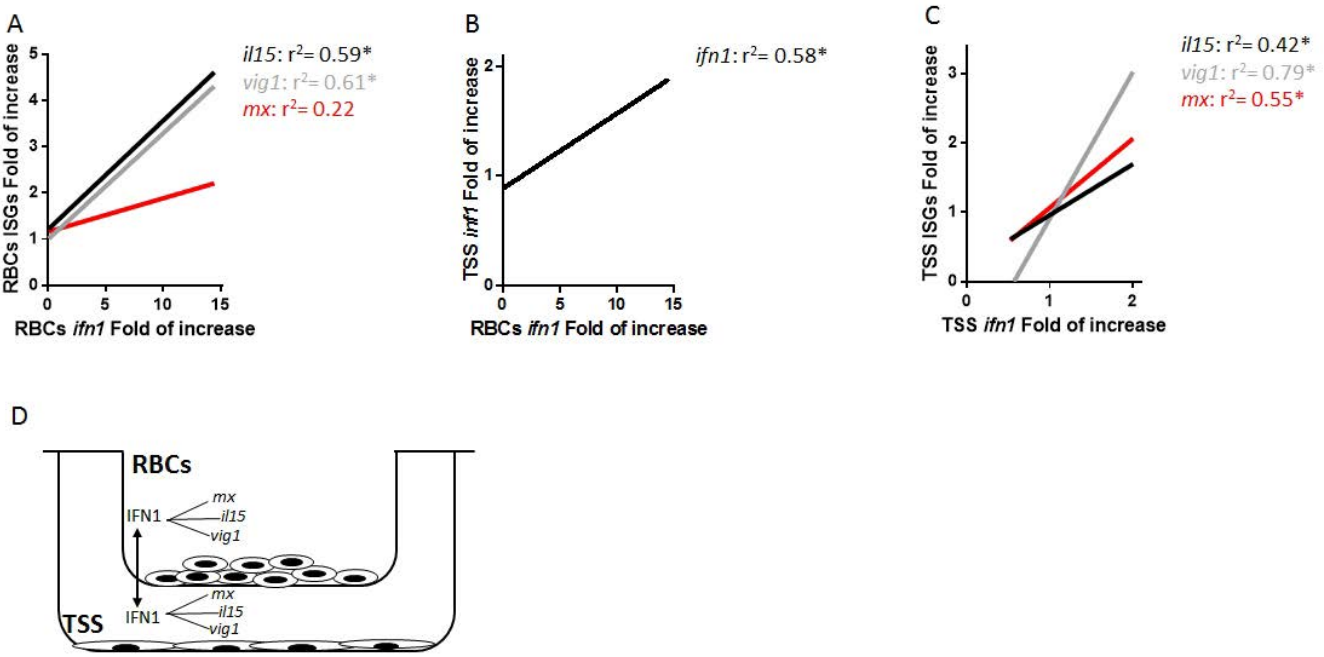

Figure 4. Crosstalk between trout RBCs and the spleen stromal cell line TSS. Control and trout RBCs stimulated with VHSV UV-inactivated, multiplicity of infection (MOI) 1, were posteriorly co-culture with TSS cell line, at 14°C, and *ifn1, mx, vig1* and *il15* gene expression profiles were quantified at 24 hours postexposure (hpe) for RBCs and TSS. (**A**) Linear regression between *ifn1* and the interferon stimulated genes (ISGs) *mx, vig1* and *il15* gene expression profiles in RBCs. (**B**) Linear regression between RBCs and TSS *ifn1* gene expression profile. (**C**) Linear regression between *ifn1* and the ISGs *mx, vig1* and *il15* gene expression profiles in TSS. Gene expression was normalized against eukaryotic 18S rRNA and relativized to control cells (red line) (fold of increase). Data is displayed as the linear regression line between the indicated cell lines and expressed genes (r^2: coefficient of determination, asterisk denote statistical significance, *P*-value < 0.05) (n = 6). (**D**) Schematic representation of the RBCs and TSS co-culture assay and analysis.

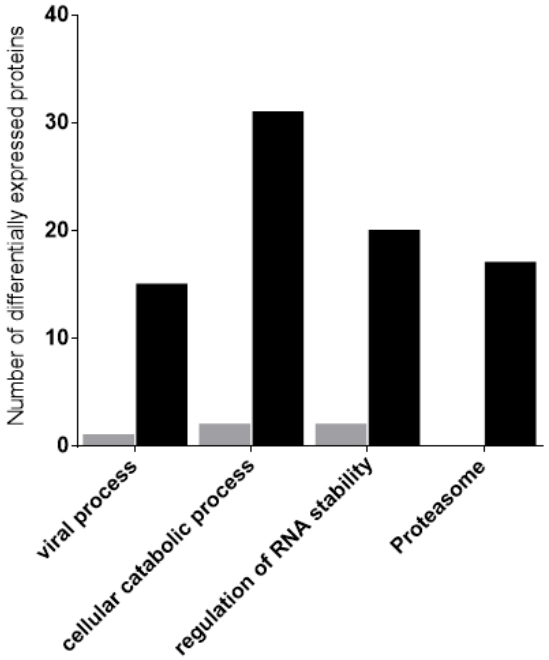

Figure 5. Gene ontology (GO) analysis of the iTRAQ-based differentially expressed proteins in VHSV-exposed trout RBCs. RBCs were exposed to VHSV with a multiplicity of infection (MOI) of 1 at 14°C. Proteins were classified into five specific GO-Biological Process categories indicated in the x-axis. The y-axis indicates the number of proteins in each category, grey bars indicate upregulated proteins and black bars down-regulated proteins.

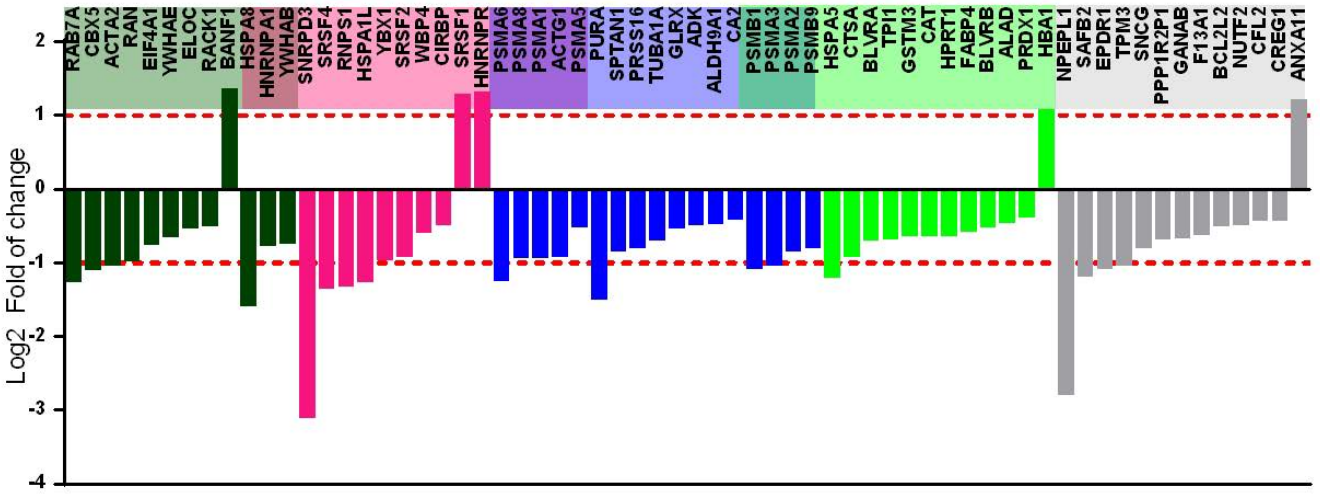

Figure 6. iTRAQ-based quantitative protein expression profile of VHSV-exposed trout RBCs. Bar plot of statistically significant differentially expressed proteins in VHSV-exposed RBCs compared to control cells (*P*-value< 0.05, FDR *q*-value < 0.05). Functional categories are labelled as follows: Blue = proteasome, pink = regulation of RNA stability, light green = cellular catabolic process, dark green= viral process, grey = proteins not associated to any function.

SNRPD3 (Small nuclear ribonucleoprotein D3 polypeptide) the most down-regulated protein with ~ -3 log2FoldChange. This protein is a core component of the spliceosomal small nuclear ribonucleoproteins (snRNPs), the building blocks of the spliceosome, and therefore, it plays an important role in the splicing of cellular pre-mRNAs. Other proteins related to splicing processes were also highly downregulated (-2>log2FoldChange>-1), such as SRSF4 (Serine/arginine-rich splicing factor 4), which plays a role in alternative splice site selection during pre-mRNA splicing, RNPS1 (RNA binding protein S1, serine-rich domain), which is part of pre- and post-splicing multiprotein messenger ribonucleoprotein (mRNP) complexes. Apart from that, several heat shock chaperones were also downregulated (-2>log2FoldChange>-1), such as HSPA1L (Heat shock 70kDa protein 1-like) and HSPA5 (Heat shock 70kDa protein 5) both involved in the correct folding of proteins and degradation of misfolded proteins, and HSPA8 (Heat shock 70kDa protein 8), which may have a scaffolding role in the spliceosome assembly. Besides, another protein highly downregulated was NPEPL1 (Aminopeptidase-like 1), a novel protein which has been implicated in HIV replication[53].

On the other hand, among the five upregulated proteins (Figure 6, Table S1), BANF1 (Barrier to Autointegration factor 1) has been directly implicated in viral processes and plays fundamental role in nuclear assembly, chromatin organization and gene expression. Besides, HNRNPR (Heterogeneous nuclear ribonucleoprotein R) plays an important role in processing precursor mRNA in the nucleus, and SRSF1 (Serine/arginine-rich splicing factor 1) is also implicated in mRNA splicing, via spliceosome.

The 59 downregulated proteins were analyzed using STRING v10.5 (RRID:SCR_005223, http://string.embl.de/)[54] with a medium confidence score threshold of 0.4. An interactome network was built for these set of proteins to find out protein-protein interaction and predict functional associations. We found that proteins within spliceosome and proteasome networks interacted with each other as well as their partners. We also found that 17 proteins were involved in viral process category and that most of them interacted with each other as well as their partners (Figure 7).

Phosphorylation of eIF2α in VHSV-exposed RBCs

Since a global protein downregulation was observed in VHSV-exposed RBCs, we further investigated whether this phenomena could be due to the phosphorylation of the α-subunit of translational initiation factor 2 (eIF2α), a recognized key mechanism of global inhibition of translational initiation. For that, phosphorylation of eIF2α (eIF2α-P) was evaluated in VHSV-exposed RBCs compared to control cells by western blot (Figure 8A and B). The results showed a small upregulation of eIF2α-P in VHSV-exposed RBCs.

Four eIF2α kinases have been identified to inhibit protein synthesis by phosphorylation of eIF2α: the double-stranded RNA-dependent eIF2α kinase (PKR), the mammalian orthologue of the yeast GCN2 protein kinase, the endoplasmic reticulum (ER) resident kinase (PERK) and heme-regulated eIF2α kinase (HRI)[55]. HRI, which was first discovered in reticulocytes under conditions of iron and heme deficiencies[56,57], was later known to regulate the synthesis of both α- and β-globins in RBCs and erythroid cells by phosphorylation of eIF2[58], and therefore inhibiting protein synthesis. Besides, heme is also known to regulate the

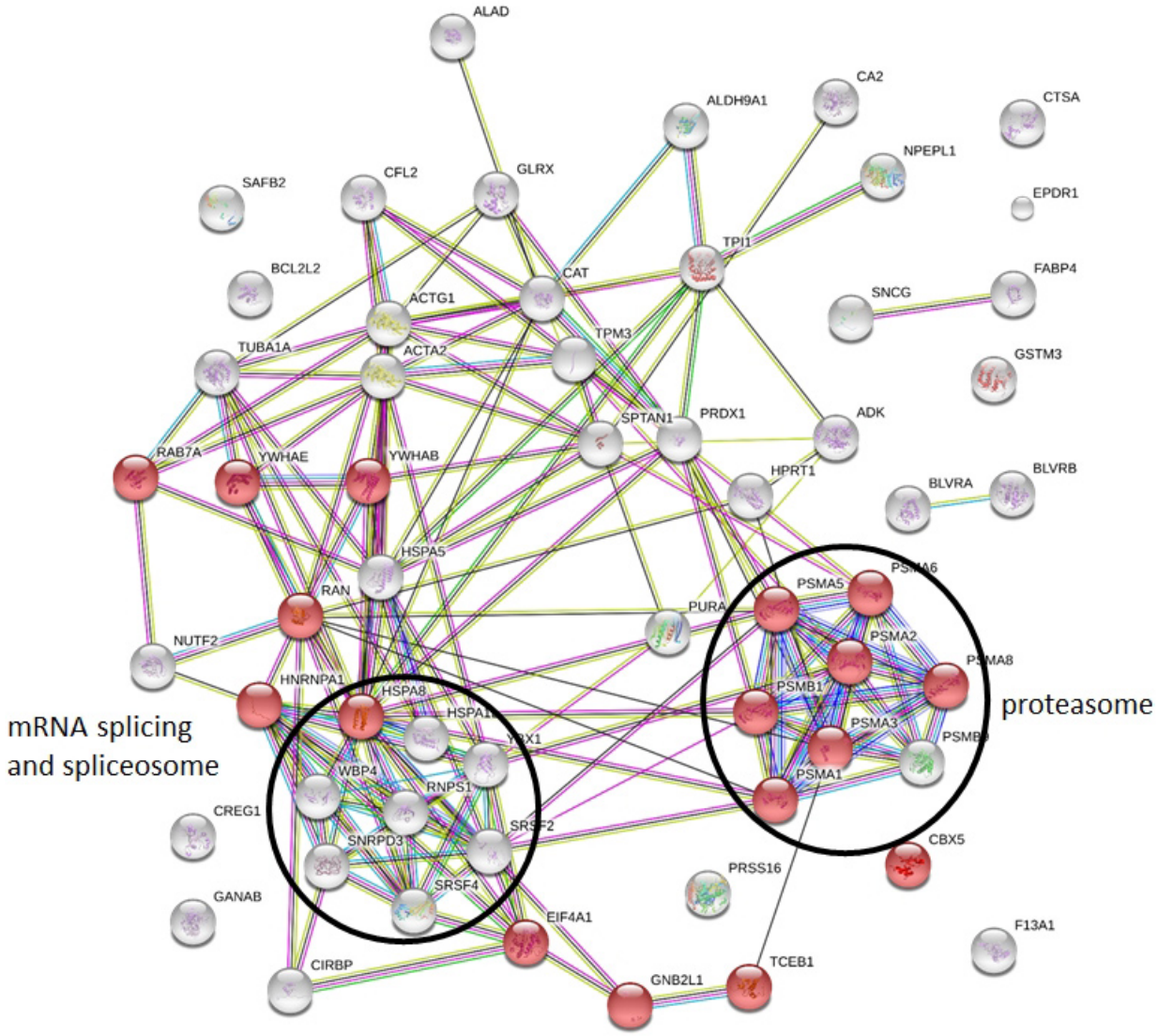

Figure 7. Constructed protein-protein interaction of the differentially downregulated proteins (DDPs) predicted using STRING software. Nodes represent DDPs and edges the interactions between two proteins. The colour of the edge indicates the interaction score (edge score). Red nodes highlight DDPs functionally annotated in viral processes.

transcription of globin genes through its binding to the transcriptional factor Bach1[59]. Taking this fact into account, we explored the RBCs *β-globin* gene expression during the course of VHSV exposure and the results showed that the *β-globin* gene was downregulated after 6 hpe (Figure 9), therefore suggesting an activation/phosphorylation of HRI and consequent phosphorylation of eIF2 and protein inhibition.

Oxidative stress and antioxidant response in VHSV-exposed RBCs

Oxidative stress is known to be induced by viral infections, being one of the major pathogenic mechanisms by altering the balance of intracellular redox[60]. On the other hand, oxidative stress is known to activate HRI, which in turn phosphorylates eIF2α and inhibits protein translation. In order to evaluate the oxidative stress induced in VHSV-exposed RBCs as a possible causative mechanism for the proteome downregulation found in our study, we examined 72 hpe the ROS intracellular production by means of DCFDA (2′,7′-Dichlorofluorescin diacetate) fluorescence intensity. The results showed that VHSV-exposed RBCs significantly augmented DCFDA fluorescent intensity 72 hpe (Figure 10A), therefore VHSV halted infection in RBCs generated oxidative stress in trout RBCs. Besides, in order to evaluate the capability of RBCs to respond to the oxidative stress, the antioxidant response of VHSV-exposed RBCs was evaluated examining the transcript levels of the antioxidant genes *fth* (ferritin), *gstp1* (glutathione S-transferase P), *nkef* (natural killer enhancement factor-like protein), *sod1* (superoxide dismutase [Cu-Zn]) and *trx* (thioredoxin).

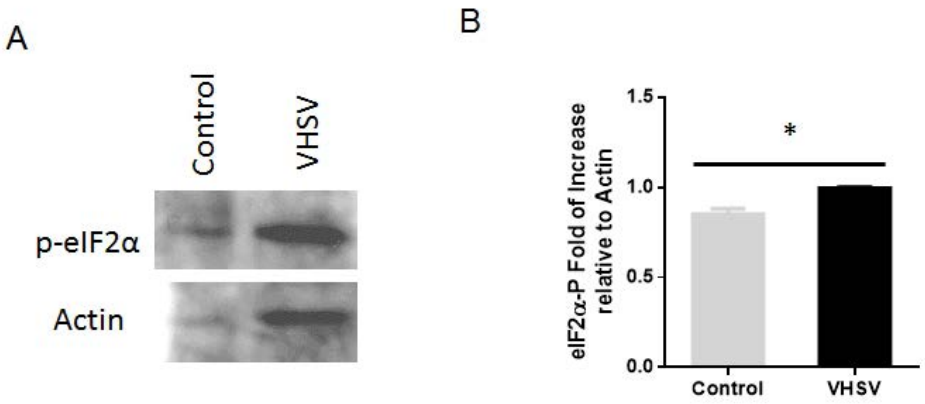

Figure 8. Phosphorylation of the translation initiation factor eIF2α in VHSV-exposed trout RBCs. (**A**) Representative western blot of eIF2α phosphorylation (eIF2α-P) in VHSV-exposed and control RBCs. **(B)** Bar plot of the eIF2α-P protein content of the stained bands estimated by densitometry, relative to α-Actin. Mann Whitney Test was performed for statistical analysis between the VHSV-exposed cells and control cells. Asterisk denote statistically significant differences (*P*-value < 0.05).

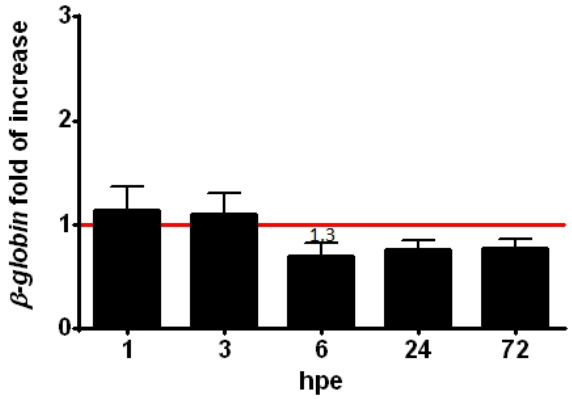

Figure 9. *β-globin* gene expression time-course in VHSV-exposed trout RBCs. RBCs were exposed to VHSV with a multiplicity of infection (MOI) of 1 at 14°C. Gene expression was quantified at time 0, 1, 3, 6, 12, 24, 72 hours postexposure (hpe). Gene expression was normalized against eukaryotic 18S rRNA and relativized to control cells (time 0, red line) (fold of increase). Data is displayed as mean ± SD (n = 3). Kruskal-Wallis Test with Dunn´s Multiple Comparison post-hoc test was performed among all conditions. Values denote pairwise significant differences with the value-indicated condition (*P*-value < 0.05).

The results depicted the increment in the transcript levels of *fth*, *gstp1*, *nkef* and *trx* (Figure 10B) as the time of exposure increased from 3 to 72 hours, demonstrating the capability of trout RBCs to counteract the oxidative stress.

Dataset 1. Excel file containing qPCR data. Each sheet contains the raw Ct values for the indicated figure numbers, organized by samples (rows) and genes (columns)

http://dx.doi.org/10.5256/f1000research.12985.d182833

Dataset 2. Excel file containing the virus titration data. Each sheet contains the virus titer (PFU/mL) results of the indicated figure number

http://dx.doi.org/10.5256/f1000research.12985.d182834

Dataset 3. Flow cytometry data. Each folder contains the Flow Cytometry Standard (.fcs) format files. Source data files are organized by figure number, and then by antibody, sample number and condition

http://dx.doi.org/10.5256/f1000research.12985.d182835

Dataset 4. Excel file containing the computed peptide spectrum match (PSM) raw data, and the spectra recovered in the iTRAQ 4-plex analysis

http://dx.doi.org/10.5256/f1000research.12985.d182836

Dataset 5. Excel file containing the iTRAQ 4-plex quantitative analysis raw data

http://dx.doi.org/10.5256/f1000research.12985.d182837

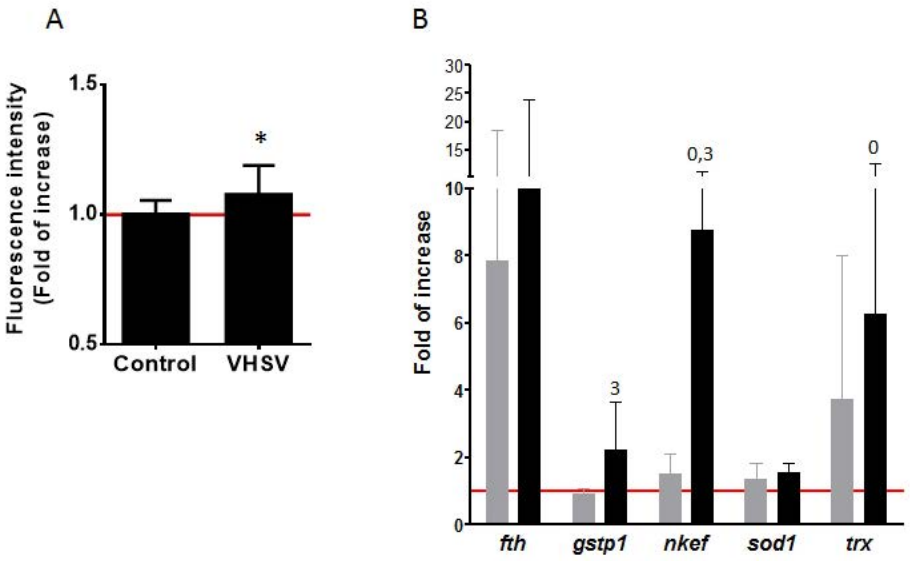

Figure 10. Effect of VHSV on ROS intracellular production and antioxidant enzymes gene expression in trout RBCs. RBCs were exposed to VHSV with a multiplicity of infection (MOI) of 1 at 14°C, (**A**) DCFDA (2′,7′-Dichlorofluorescin diacetate) fluorescence intensity of VHSV-exposed RBCs relative to control cells, 72 hours postexposure (hpe). (**B**) Antioxidant genes (*fth*: ferritin, *gstp1*: glutathione S-transferase P, *nkef:* natural killer enhancement factor-like protein, *sod1*: superoxide dismutase [Cu-Zn], *trx*: thioredoxin) gene expression quantified 72 hpe. Gene expression was normalized against eukaryotic 18S rRNA and relativized to control cells (time 0, red line) (fold of increase). Data is displayed as mean ± SD (n = 3). Kruskal-Wallis Test with Dunn´s Multiple Comparison post-hoc test was performed among all conditions. Values denote pairwise significant differences (*P*-value < 0.05) with the value-indicated condition.

Dataset 6. Excel file containing the densitometry raw data of eIF2α-P and α-Actin western blots. Related uncropped blots are included

http://dx.doi.org/10.5256/f1000research.12985.d182838

Dataset 7. Excel file containing DCFDA absorbance raw data

http://dx.doi.org/10.5256/f1000research.12985.d182839

Discussion

Most viral infections release their progeny to the outside of the cells (productive infections). However, viral infections can be also non-productive in non-permissive cells (also called abortive). Viral abortive infections occur when a virus enters a host-cell, then some or all viral components are synthesized but finally no infective viruses are released[61]. This situation may result from an infection with defective viruses or because the host cell is non-permissive and inhibits replication of a particular virus. Our results are consistent with VHSV binding and internalization, followed by viral genes transcription at early times of viral exposure and posterior quasi-inhibition inside trout RBCs. In this sense, trout RBCs could be classified as a non-permissive cell for VHSV replication, in contrast to other trout cells or tissues where VHSV is productive, such as RTG-2 cells[62,63], fin cells[64] or stroma[65]. Therefore, from our results, VHSV infection could be classified as halted in trout RBCs, since it enters the cell, but do not replicate at the levels comparable to the ~100-fold increase in titre of PRV and ISAV infections in salmon RBCs[8,10]. In fact, an apparent inhibition of the early viral genes transcription seemed to occur since N_{VHSV}: G_{VHSV} viral genes transcripts ratio was very low, and therefore did not follow the attenuation phenomenon found in rhabdoviruses[45]. However, strikingly, even though the recovered VHSV titer in the RBCs supernatant was very low 3 and 6 dpe, at 40 dpe almost the same virus titer could be recovered from the RBCs supernatant (data not shown), suggesting an *ex vivo* persistence of the halted VHSV inside RBCs.

In the literature, innate immune responses have been associated with viral abortive infections, including rhabdoviruses. Pham *et al.*[66] speculated that the cause of the aborted VHSV infection in a trout macrophage cell line (RTS-11) could be the constitutive expression and/or upregulation of the *mx* genes. The abortive infection of the snakehead fish vesiculovirus (SHVV) in a zebrafish embryonic fibroblast cell line (ZF4) was associated with the activation of Retinoic acid-Inducible Gene I (RIG-I)-like receptors and interferon pathway by viral replicative intermediates[67]. Similarly, in mammals, Pfefferkorn *et al.*[68] demonstrated that the abortive viral infection of astrocytes by rabies virus (RABV) and vesicular stomatitis virus (VSV) triggered a pattern recognition receptor signaling, which resulted in the secretion of IFN-β. On the other hand, it has been also described that alveolar macrophages are able to restrict the respiratory syncytial virus (RSV) replication even in the absence of type I IFNs (IFN1)[69]. In this sense, VHSV halted infection in trout RBCs did not seem to be related to IFN1 or IFN1-inducible genes, since *inf1*, *mx* and *pkr* genes as well as Mx and IFN1 proteins appeared poorly modulated or downregulated during VHSV exposure, in contrary to the 8-fold increase in ISAV productive infection in

salmon RBCs[10], the 50-fold increases in PRV productive infection in salmon RBCs[8] or the 50-fold increases in IPNV non-productive infection in rainbow trout RBCs (unpublished study, Nombela I, Carrion A, Puente-Marin S, Chico V, Mercado L, Perez L, Coll J, and Ortega-Villaizan M). Alternatively, the high levels of constitutive Mx protein expression might have prevented its further increase in VHSV-exposed RBCs, like it is the case of the rainbow trout monocyte-macrophage RTS-11 cell line[70]. On the other hand, several cell mechanisms have been reported to suppress IFN1-mediated responses, which include downregulation of cell surface IFNα receptor (IFNAR) expression, induction of negative regulators (such as suppressor of cytokine signalling (SOCS) proteins and ubiquitin carboxy-terminal hydrolase 18 (USP18)), as part of a negative feedback loop to limit the extent and duration of IFN1 responses[71]. Separately, a putative antagonistic effect of the VHSV virus on the Mx induction has been previously reported[72,73]. Thus, it has been reported that VHSV NV protein interferes with the IFN signalling pathway, resulting in a poor induction of the Japanese flounder Mx promoter[74]. Furthermore, a lack of Mx upregulation has been speculated to be due to the immunosuppression caused by VHSV NV in trout injected with recombinant NV[75]. Recently, VHSV M protein has been also reported to suppress IFN1-induced gene expression[76]. From our results, in VHSV-exposed RBCs, the *mx* gene poor induction or slight downregulation could be probably supported by the existence of a VHSV antagonistic effect against the RBCs IFN response. To further clarify whether a viral antagonistic effect or a feedback loop of IFN1 and/or IFN1-inducible genes induction is related to or responsible for aborting or halting viral infections in trout RBCs remains to be studied, and are part of our ongoing research.

Separately, although the IFN levels were low, our results demonstrated the paracrine IFN crosstalk between RBCs, stimulated with UV-inactivated VHSV, and the spleen stromal the TSS cell line. The TSS cell line has been described to resemble the immune responses observed in cultures of head kidney macrophages[77]. Also, it has been demonstrated the ability of TSS to positively respond to conditioned supernatants from head kidney macrophage cultures exposed to poly I:C[77]. As well, after exposure to poly I:C, TSS produced a high upregulation of the Mx-1 gene[78]. Our results showed the correlated *ifn1* regulation in both cell lines, as well as by the correlative regulation of the interferon-inducible *mx* gene in TSS, the regulation of *il15*, an interleukin that can activate antiviral responses via an interferon-dependent mechanism[79], and the VHSV-inducible *vig1*, a gene induced by VHSV as well as by interferon[80]. Therefore, this crosstalk demonstrated the capacity of trout RBCs to exert a paracrine molecular antiviral communication with other cells with capacity to generate an immune response, as it is the case of the TSS cell line[78]. However, more extended research is need to identify further molecules involved in this crosstalk.

On the other hand, other immune proteins, such as BD1, IL1β and IL8, known to be involved in antiviral immunity, which were upregulated in VHSV- exposed RBCs, appeared to be part of the antiviral immune response of trout RBCs and could be implicated in the halted viral replication inside RBCs.

To further investigate the mechanisms implicated in the immune response of trout RBCs to VHSV, the comprehensive analysis of the differentially expressed proteins, obtained by means of iTRAQ proteome profiling, revealed the regulation of two typical mechanisms for viral subversive strategies: regulation of spliceosome, or splicing hijacking, and host-cell shut-off. However, even though these strategies usually lead to viral augmented replication and cell death, in the case of VHSV-exposed RBCs this is not observed. Therefore, how these strategies or another strategies contribute to halting viral replication yet remains elusive. Future research could be directed to investigate the role/implication of the small nuclear ribonucleoprotein SNRPD3, the aminopeptidase NPEPL1, the serine/arginine-rich splicing factor SRSF1 and the heterogeneous nuclear ribonucleoprotein HNRNPR, in the response of RBCs against VHSV replication, since these proteins were the more regulated ones and they have been shown to be implicated in HIV replication[53,81–83]).

It is noticeable that the iTRAQ-based protein profiling could not detect cytokines or other molecules related to the antiviral immune response, which could be detected by RT-qPCR, FC or IF. This fact could be due to the idiosyncratic limitations of the iTRAQ technique, such as its tendency to underestimate quantifications[84], especially for low-represented proteins. This fact becomes especially critical in the case of RBC proteome analysis, since their protein production is lower compared to other cells. Further protein profiling by means of label-free protein quantification is ongoing.

On the other hand, the inhibition of both host and viral translation has been shown during infection with the prototype rhabdovirus vesicular stomatitis virus (VSV)[85]. During VSV infection, there is a rapid inhibition of host mRNA translation early after infection, followed by a later inhibition of viral mRNA translation, which has been associated to eIF2α phosphorylation[86]. Our results showed a slight increment in eIF2α phosphorylation in VHSV-exposed RBCs, indicating that this mechanism could be implicated in the inhibition of VHSV replication in trout RBCs. In this context, HRI, the heme-regulated eIF2α kinase, is one of the four kinases identified to inhibit protein synthesis by means of eIF2α phosphorylation. HRI is predominantly expressed in reticulocytes and erythroid precursors[56,57], and it is known to regulate the synthesis of both α- and β-globins in RBCs and erythroid cells by phosphorylation of eIF2[58]. Moreover, heme, the prosthetic group of hemoglobin, is known to inhibit eIF2α and therefore the transcription of globin genes through its binding to the transcriptional factor Bach1. From our results, we observed a decrease in the *β-globin* gene transcripts levels during the course of viral exposure, which accompanied with the observed phosphorylation of eIF2α could suggest a possible heme regulation mechanism of eIF2 pathway in response to VHSV exposure in trout RBCs. The mechanism by which heme is altered in trout RBCs during VHSV exposure remains to be investigated.

Another interesting mechanism found in trout RBCs in response to VHSV was the implication of the protective antioxidant enzymes genes *fth*, *gstp1*, *nkef* and *trx* in the defense of RBCs against the induction of ROS after VHSV exposure, since as the

course of exposure increased, ROS slightly augmented in parallel to the transcript levels of these enzymes. These systems are known to contribute not only to repair the oxidative damage maintaining redox homeostasis, but also to the overall response of the cell to ROS by acting as oxidative sensors in signal transduction pathways[87]. Besides, regarding the implication of antioxidants activity against viral replication, it has been described that antioxidants can suppress virus-induced oxidative stress and reduce RNA virus production[88]. Separately, these antioxidant enzymes are known NF-κβ antioxidant targets in response to inflammation stimulus (reviewed in Morgan and Liu, 2011[87]) and ROS can be sometimes produced in response to cytokines. Since NF-κβ appeared slightly activated in VHSV-exposed RBCs (Figure S3A and B), it is suggested that the cytokine response generated after VHSV exposure in trout RBCs would induce ROS production, and in turn this would modulate the NF-κβ response and NF-κβ target genes could attenuate ROS to promote RBCs survival. Apart from the observation of NF-κβ translocation to the nucleus in some of the RBCs, it is noteworthy that it is always accompanied by an increase in the protein levels of the p65 NF-κβ subunit in the cytoplasm. This phenomenon has been also observed in human foreskin fibroblasts during HCMV infection, where an increase in p65 mRNA levels correlated with the sustained increase in NF-kB activity during the course of infection[89]. On the other hand, the nuclear factor-erythroid 2 related factor 2 (Nrf2) and its downstream genes (i.e. Heme Oxygenase-1, HO1 and thrioredoxin) are also known as master genes of cellular defense against oxidative stress by scavenging ROS. Another fish rhabdovirus, the SVCV, has been reported to induce accumulation of ROS accompanied by the up-regulation of Nrf2 and its downstream genes. The overexpression of Nrf2 has been also reported to significantly suppress either entry or replication of several viruses (reviewed in 90), and Shao *et al.*[90] also demonstrated that the activation of Nrf2 repressed the replication of SVCV. Therefore, future research could be directed to investigate the implication of the Nrf2 pathway in inhibiting VHSV replication in trout RBCs.

It is evident that the antiviral response of RBCs is low compared to other cells of the immune system. However, this fact could be explained by the inherent characteristic of the RBCs as the most abundant cell in the blood, where a unanimous high cytokine response by RBCs could lead to a septic shock. On the other hand, it is also noticeable the high inter-individual variability found for most of the genes and proteins assayed, which could be explained by the idiosyncratic presence of immune responders and non-responders in every assay.

In summary, this study unveils previously unobserved but important mechanisms for fish nucleated RBCs in the contribution to the defense against a viral aggression not involving RBCs as targets. To our knowledge, this is the first report that implicates fish RBCs as antiviral mediators against viruses targeting other tissues or cells. The recognition of body circulating viruses and the subsequent generation of immune defenses by RBCs may largely contribute to fish survival, given the large volume of RBCs and its rapid and wide distribution to the whole body. We are further investigating if similar mechanisms operate *in vivo*, the molecules that trigger such immune responses or the cellular factors implicated in the interaction with the virus.

Data availability

F1000Research: Dataset 1. Excel file containing qPCR data. Each sheet contains the raw Ct values for the indicated figure numbers, organized by samples (rows) and genes (columns), 10.5256/f1000research.12985.d182833[93]

F1000Research: Dataset 2. Excel file containing the virus titration data. Each sheet contains the virus titer (PFU/mL) results of the indicated figure number, 10.5256/f1000research.12985.d182834[94]

F1000Research: Dataset 3. Flow cytometry data. Each folder contains the Flow Cytometry Standard (.fcs) format files. Source data files are organized by figure number, and then by antibody, sample number and condition, 10.5256/f1000research.12985.d182835[95]

F1000Research: Dataset 4. Excel file containing the computed peptide spectrum match (PSM) raw data, and the spectra recovered in the iTRAQ 4-plex analysis., 10.5256/f1000research.12985.d182836[96]

F1000Research: Dataset 5. Excel file containing the iTRAQ 4-plex quantitative analysis raw data., 10.5256/f1000research.12985.d182837[97]

F1000Research: Dataset 6. Excel file containing the densitometry raw data of eIF2α-P and α-Actin western blots. Related uncropped blots are included., 10.5256/f1000research.12985.d182838[98]

F1000Research: Dataset 7. Excel file containing DCFDA absorbance raw data., 10.5256/f1000research.12985.d182839[99]

Competing interests

No competing interests were disclosed.

Grant information

This work was supported by the European Research Council (ERC starting grant 2014 GA639249).

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Acknowledgements

Special acknowledgment is due to the co-author Dr. Amparo Estepa, passed away, who largely contributed to the initial ideas and enthusiasm behind this work. Thanks are due also to Beatriz Bonmati, Remedios Torres and Efren Lucas for their technical assistance. As well, thanks are due to Prof. Henny Gevers and Dr. Craig Plaisance for helping with English editing.

Supplementary material

Figure S1. Representative flow cytometry dotplots of immune protein responses of VHSV-exposed RBCs. RBCs were exposed to VHSV at MOI 1, at 14°C, and stained with anti-BD1 (**A**) and anti-IL8 (**B**), 72 hpe. Control and VHSV-exposed RBCs dotplots are shown. Y axis represents side scattering (SSC-A) and X axis FITC fluorescence intensity (FITC-A).

Click here to access the data.

Figure S2. Pathway network of significantly over-represented GO-terms in VHSV-exposed trout RBCs protein iTRAQ profiling. Big nodes represent significantly differentially expressed (down-regulated) proteins that have similar function; edges represent pairwise interactions; small nodes represent the proteins associated to each function. Functional groups are labelled as follows: Blue = proteasome, pink = regulation of RNA stability, light green = cellular catabolic process, dark green= viral process, grey = proteins not associated to any function. A list of all over-represented terms is provided in Table S1.

Click here to access the data.

Figure S3. NF-kß p65 protein labelling in VHSV-exposed RBCs. (**A**) Protein expression levels calculated by the formula MRFI (Mean Relative Fluorescence Intensity) = fluorescence in VHSV-exposed RBCs / fluorescence in non-exposed RBCs, at MOI 1, 10 and 100, 72hpe, at 14°C, relative to control cells (red line). Data represent mean ± SD (n=3). Mann Whitney Test was performed for statistical analysis between the VHSV-exposed cells and control cells. (**B**) Representative immunofluorescences of control and VHSV-exposed RBCs stained with anti-NF-kß (FITC) and DAPI for nuclei (IF representative of 20 images).

Click here to access the data.

Table S1. List of significantly over-represented GO-terms in VHSV-exposed trout RBCs protein iTRAQ profiling.

Click here to access the data.

References

1. Magadan S, Sunyer OJ, Boudinot P: **Unique Features of Fish Immune Repertoires: Particularities of Adaptive Immunity Within the Largest Group of Vertebrates.** *Results Probl Cell Differ.* 2015; **57**: 235–64.
PubMed Abstract | Publisher Full Text | Free Full Text
2. Sunyer JO: **Fishing for mammalian paradigms in the teleost immune system.** *Nat Immunol.* 2013; **14**(4): 320–6.
PubMed Abstract | Publisher Full Text | Free Full Text
3. Li J, Barreda DR, Zhang YA, *et al.*: **B lymphocytes from early vertebrates have potent phagocytic and microbicidal abilities.** *Nat Immunol.* 2006; **7**(10): 1116–24.
PubMed Abstract | Publisher Full Text
4. Estepa A, Coll J: **Innate Multigene Family Memories Are Implicated in the Viral-Survivor Zebrafish Phenotype.** *PLoS One.* 2015; **10**(8): e0135483.
PubMed Abstract | Publisher Full Text | Free Full Text
5. Morera D, Roher N, Ribas L, *et al.*: **RNA-Seq reveals an integrated immune response in nucleated erythrocytes.** *PLoS One.* 2011; **6**(10): e26998.
PubMed Abstract | Publisher Full Text | Free Full Text
6. Morera D, Mackenzie SA: **Is there a direct role for erythrocytes in the immune response?** *Vet Res.* 2011; **42**(1): 89.
PubMed Abstract | Publisher Full Text | Free Full Text
7. Passantino L, Altamura M, Cianciotta A, *et al.*: **Maturation of fish erythrocytes coincides with changes in their morphology, enhanced ability to interact with *Candida albicans* and release of cytokine-like factors active upon autologous macrophages.** *Immunopharmacol Immunotoxicol.* 2004; **26**(4): 573–85.
PubMed Abstract | Publisher Full Text
8. Wessel Ø, Olsen CM, Rimstad E, *et al.*: **Piscine orthoreovirus (PRV) replicates in Atlantic salmon (*Salmo salar* L.) erythrocytes *ex vivo*.** *Vet Res.* 2015; **46**: 26.
PubMed Abstract | Publisher Full Text | Free Full Text
9. Dahle MK, Wessel Ø, Timmerhaus G, *et al.*: **Transcriptome analyses of Atlantic salmon (*Salmo salar* L.) erythrocytes infected with piscine orthoreovirus (PRV).** *Fish Shellfish Immunol.* 2015; **45**(2): 780–90.
PubMed Abstract | Publisher Full Text
10. Workenhe ST, Kibenge MJ, Wright GM, *et al.*: **Infectious salmon anaemia virus replication and induction of alpha interferon in Atlantic salmon erythrocytes.** *Virol J.* 2008; **5**: 36.
PubMed Abstract | Publisher Full Text | Free Full Text
11. Dhar AK, Manna SK, Thomas Allnutt FC: **Viral vaccines for farmed finfish.** *Virusdisease.* 2014; **25**(1): 1–17.
PubMed Abstract | Publisher Full Text | Free Full Text
12. Schütze H, Mundt E, Mettenleiter TC: **Complete genomic sequence of viral hemorrhagic septicemia virus, a fish rhabdovirus.** *Virus Genes.* 1999; **19**(1): 59–65.
PubMed Abstract | Publisher Full Text
13. Bang Jensen B, Kristoffersen AB: **Risk factors for outbreaks of infectious pancreatic necrosis (IPN) and associated mortality in Norwegian salmonid farming.** *Dis Aquat Organ.* 2015; **114**(3): 177–87.
PubMed Abstract | Publisher Full Text
14. Daher KA, Selsted ME, Lehrer RI: **Direct inactivation of viruses by human granulocyte defensins.** *J Virol.* 1986; **60**(3): 1068–74.
PubMed Abstract | Free Full Text
15. Falco A, Mas V, Tafalla C, *et al.*: **Dual antiviral activity of human alpha-defensin-1 against viral haemorrhagic septicaemia rhabdovirus (VHSV): inactivation of virus particles and induction of a type I interferon-related response.** *Antiviral Res.* 2007; **76**(2): 111–23.
PubMed Abstract | Publisher Full Text
16. Chico V, Martinez-Lopez A, Ortega-Villaizan M, *et al.*: **Pepscan mapping of viral hemorrhagic septicemia virus glycoprotein G major lineal determinants implicated in triggering host cell antiviral responses mediated by type I interferon.** *J Virol.* 2010; **84**(14): 7140–50.
PubMed Abstract | Publisher Full Text | Free Full Text
17. Martinez-Lopez A, Garcia-Valtanen P, Ortega-Villaizan M, *et al.*: **VHSV G glycoprotein major determinants implicated in triggering the host type I IFN antiviral response as DNA vaccine molecular adjuvants.** *Vaccine.* 2014; **32**(45): 6012–9.
PubMed Abstract | Publisher Full Text
18. Rojas V, Camus-Guerra H, Guzmán F, *et al.*: **Pro-inflammatory caspase-1 activation during the immune response in cells from rainbow trout *Oncorhynchus mykiss* (Walbaum 1792) challenged with pathogen-associated molecular patterns.** *J Fish Dis.* 2015; **38**(11): 993–1003.
PubMed Abstract | Publisher Full Text
19. Schmitt P, Wacyk J, Morales-Lange B, *et al.*: **Immunomodulatory effect of cathelicidins in response to a β-glucan in intestinal epithelial cells from rainbow trout.** *Dev Comp Immunol.* 2015; **51**(1): 160–9.
PubMed Abstract | Publisher Full Text

20. Santana P, Palacios C, Narváez E, *et al.*: **Anti-peptide antibodies: A tool for detecting IL-8 in salmonids.** *Electron J Biotechnol.* 2012; **15**(5).
Publisher Full Text

21. Rojas V, Morales-Lange B, Guzmán F, *et al.*: **Immunological strategy for detecting the pro-inflammatory cytokine TNF-alpha in salmonids.** *Electron J Biotechnol.* 2012; **15**(5).
Publisher Full Text

22. Santana PA, Álvarez CA, Guzmán F, *et al.*: **Development of a sandwich ELISA for quantifying hepcidin in Rainbow trout.** *Fish Shellfish Immunol.* 2013; **35**(3): 748–55.
PubMed Abstract | Publisher Full Text

23. Bethke J, Rojas V, Berendsen J, *et al.*: **Development of a new antibody for detecting natural killer enhancing factor (NKEF)-like protein in infected salmonids.** *J Fish Dis.* 2012; **35**(5): 379–88.
PubMed Abstract | Publisher Full Text

24. Encinas P, Garcia-Valtanen P, Chinchilla B, *et al.*: **Identification of multipath genes differentially expressed in pathway-targeted microarrays in zebrafish infected and surviving spring viremia carp virus (SVCV) suggest preventive drug candidates.** *PLoS One.* 2013; **8**(9): e73553.
PubMed Abstract | Publisher Full Text | Free Full Text

25. García-Valtanen P, Martinez-Lopez A, Ortega-Villaizan M, *et al.*: **In addition to its antiviral and immunomodulatory properties, the zebrafish β-defensin 2 (zfBD2) is a potent viral DNA vaccine molecular adjuvant.** *Antiviral Res.* 2014; **101**: 136–47.
PubMed Abstract | Publisher Full Text

26. Abós B, Castro R, González Granja A, *et al.*: **Early activation of teleost B cells in response to rhabdovirus infection.** *J Virol.* 2015; **89**(3): 1768–80.
PubMed Abstract | Publisher Full Text | Free Full Text

27. Sanz F, Basurco B, Babin M, *et al.*: **Monoclonal antibodies against the structural proteins of viral haemorrhagic septicaemia virus isolates.** *J Fish Dis.* 1993; **16**(1): 53–63.
Publisher Full Text

28. Carracedo B: **Caracterización de cultivos celulares angiogénicos obtenidos de órganos linfoides de trucha arco iris, Oncorhynchus mykiss.** Ph.D. thesis: University of León. Spain. 2003.

29. Winton J, Batts W, deKinkelin P, *et al.*: **Current lineages of the e*pithelioma papulosum cyprini* (EPC) cell line are contaminated with fathead minnow, *Pimephales promela*s, cells.** *J Fish Dis.* 2010; **33**(8): 701–4.
PubMed Abstract | Publisher Full Text

30. LeBerre M, De Kinkelin P, Metzger A: **Identification sérologique des rhabdovirus des salmonidés.** *Bull Off Int Epizoot.* 1977; **87**: 391–3.
Reference Source

31. Basurco B, Coll JM: **Spanish isolates and reference strains of viral haemorrhagic septicaemia virus shown similar protein size patterns.** *Bull Eur Ass Fish Pathol.* 1989; **9**(4): 92–5.
Reference Source

32. Mas V, Pérez L, Encinar JA, *et al.*: **Salmonid viral haemorrhagic septicaemia virus: fusion-related enhancement of virus infectivity by peptides derived from viral glycoprotein G or a combinatorial library.** *J Gen Virol.* 2002; **83**(Pt 11): 2671–81.
PubMed Abstract | Publisher Full Text

33. García-Valtanen P, Ortega-Villaizán Mdel M, Martínez-López A, *et al.*: **Autophagy-inducing peptides from mammalian VSV and fish VHSV rhabdoviral G glycoproteins (G) as models for the development of new therapeutic molecules.** *Autophagy.* 2014; **10**(9): 1666–80.
PubMed Abstract | Publisher Full Text | Free Full Text

34. Chico V, Gomez N, Estepa A, *et al.*: **Rapid detection and quantitation of viral hemorrhagic septicemia virus in experimentally challenged rainbow trout by real-time RT-PCR.** *J Virol Methods.* 2006; **132**(1–2): 154–9.
PubMed Abstract | Publisher Full Text

35. Livak KJ, Schmittgen TD: **Analysis of relative gene expression data using real-time quantitative PCR and the $2^{-\Delta\Delta C}_{T}$ Method.** *Methods.* 2001; **25**(4): 402–8.
PubMed Abstract | Publisher Full Text

36. Walpurgis K, Kohler M, Thomas A, *et al.*: **Validated hemoglobin-depletion approach for red blood cell lysate proteome analysis by means of 2D PAGE and Orbitrap MS.** *Electrophoresis.* 2012; **33**(16): 2537–45.
PubMed Abstract | Publisher Full Text

37. Geer LY, Markey SP, Kowalak JA, *et al.*: **Open mass spectrometry search algorithm.** *J Proteome Res.* 2004; **3**(5): 958–64.
PubMed Abstract | Publisher Full Text

38. Craig R, Beavis RC: **TANDEM: matching proteins with tandem mass spectra.** *Bioinformatics.* 2004; **20**(9): 1466–7.
PubMed Abstract | Publisher Full Text

39. Tabb DL, Fernando CG, Chambers MC: **MyriMatch: highly accurate tandem mass spectral peptide identification by multivariate hypergeometric analysis.** *J Proteome Res.* 2007; **6**(2): 654–61.
PubMed Abstract | Publisher Full Text | Free Full Text

40. Ramos-Fernández A, Paradela A, Navajas R, *et al.*: **Generalized method for probability-based peptide and protein identification from tandem mass spectrometry data and sequence database searching.** *Mol Cell Proteomics.* 2008; **7**(9): 1748–54.
PubMed Abstract | Publisher Full Text | Free Full Text

41. Lopez-Serra P, Marcilla M, Villanueva A, *et al.*: **A *DERL3*-associated defect in the degradation of SLC2A1 mediates the Warburg effect.** *Nat Commun.* 2014; **5**: 3608.
PubMed Abstract | Publisher Full Text | Free Full Text

42. Bindea G, Mlecnik B, Hackl H, *et al.*: **ClueGO: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks.** *Bioinformatics.* 2009; **25**(8): 1091–3.
PubMed Abstract | Publisher Full Text | Free Full Text

43. Bindea G, Galon J, Mlecnik B: **CluePedia Cytoscape plugin: pathway insights using integrated experimental and *in silico* data.** *Bioinformatics.* 2013; **29**(5): 661–3.
PubMed Abstract | Publisher Full Text | Free Full Text

44. Shannon P, Markiel A, Ozier O, *et al.*: **Cytoscape: a software environment for integrated models of biomolecular interaction networks.** *Genome Res.* 2003; **13**(11): 2498–504.
PubMed Abstract | Publisher Full Text | Free Full Text

45. Banerjee AK: **Transcription and replication of rhabdoviruses.** *Microbiol Rev.* 1987; **51**(1): 66–87.
PubMed Abstract | Free Full Text

46. Mas V, Rocha A, Perez L, *et al.*: **Reversible inhibition of spreading of *in vitro* infection and imbalance of viral protein accumulation at low pH in viral hemorrhagic septicemia rhabdovirus, a salmonid rhabdovirus.** *J Virol.* 2004; **78**(4): 1936–44.
PubMed Abstract | Publisher Full Text | Free Full Text

47. Schloemer RH, Wagner RR: **Cellular adsorption function of the sialoglycoprotein of vesicular stomatitis virus and its neuraminic acid.** *J Virol.* 1975; **15**(4): 882–93.
PubMed Abstract | Free Full Text

48. Oksayan S, Nikolic J, David CT, *et al.*: **Identification of a role for nucleolin in rabies virus infection.** *J Virol.* 2015; **89**(3): 1939–43.
PubMed Abstract | Publisher Full Text | Free Full Text

49. Choi MK, Moon CH, Ko MS, *et al.*: **A nuclear localization of the infectious haematopoietic necrosis virus NV protein is necessary for optimal viral growth.** *PLoS One.* 2011; **6**(7): e22362.
PubMed Abstract | Publisher Full Text | Free Full Text

50. Catton WT: **Blood cell formation in certain teleost fishes.** *Blood.* 1951; **6**(1): 39–60.
PubMed Abstract

51. Fänge R, Nilsson S: **The fish spleen: structure and function.** *Experientia.* 1985; **41**(2): 152–8.
PubMed Abstract | Publisher Full Text

52. Ganassin RC, Bols NC: **A stromal cell line from rainbow trout spleen, RTS34ST, that supports the growth of rainbow trout macrophages and produces conditioned medium with mitogenic effects on leukocytes.** *In Vitro Cell Dev Biol Anim.* 1999; **35**(2): 80–6.
PubMed Abstract | Publisher Full Text

53. Liu L, Oliveira NM, Cheney KM, *et al.*: **A whole genome screen for HIV restriction factors.** *Retrovirology.* 2011; **8**: 94.
PubMed Abstract | Publisher Full Text | Free Full Text

54. Szklarczyk D, Franceschini A, Wyder S, *et al.*: **STRING v10: protein-protein interaction networks, integrated over the tree of life.** *Nucleic Acids Res.* 2015; **43**(Database issue): D447–52.
PubMed Abstract | Publisher Full Text | Free Full Text

55. Han AP, Yu C, Lu L, *et al.*: **Heme-regulated eIF2alpha kinase (HRI) is required for translational regulation and survival of erythroid precursors in iron deficiency.** *EMBO J.* 2001; **20**(23): 6909–18.
PubMed Abstract | Publisher Full Text | Free Full Text

56. Grayzel AI, Hörchner P, London IM: **The stimulation of globin synthesis by heme.** *Proc Natl Acad Sci U S A.* 1966; **55**(3): 650–5.
PubMed Abstract | Publisher Full Text | Free Full Text

57. Legon S, Jackson RJ, Hunt T: **Control of protein synthesis in reticulocyte lysates by haemin.** *Nat New Biol.* 1973; **241**(109): 150–2.
PubMed Abstract | Publisher Full Text

58. Chen JJ: **Regulation of protein synthesis by the heme-regulated eIF2alpha kinase: relevance to anemias.** *Blood.* 2007; **109**(7): 2693–9.
PubMed Abstract | Publisher Full Text | Free Full Text

59. Tahara T, Sun J, Igarashi K, *et al.*: **Heme-dependent up-regulation of the alpha-globin gene expression by transcriptional repressor Bach1 in erythroid cells.** *Biochem Biophys Res Commun.* 2004; **324**(1): 77–85.
PubMed Abstract | Publisher Full Text

60. Camini FC, da Silva Caetano CC, Almeida LT, *et al.*: **Implications of oxidative stress on viral pathogenesis.** *Arch Virol.* 2017; **162**(4): 907–17.
PubMed Abstract | Publisher Full Text

61. Boukhvalova MS, Prince GA, Blanco JC: **Respiratory syncytial virus infects and abortively replicates in the lungs in spite of preexisting immunity.** *J Virol.* 2007; **81**(17): 9443–50.
PubMed Abstract | Publisher Full Text | Free Full Text

62. Cano I, Collet B, Pereira C, *et al.*: ***In vivo* virulence of viral haemorrhagic septicaemia virus (VHSV) in rainbow trout Oncorhynchus mykiss correlates inversely with *in vitro* Mx gene expression.** *Vet Microbiol.* 2016; **187**: 31–40.
PubMed Abstract | Publisher Full Text

63. Lorenzen E, Carstensen B, Olesen NJ: **Inter-laboratory comparison of cell lines for susceptibility to three viruses: VHSV, IHNV and IPNV.** *Dis Aquat Organ.* 1999; **37**(2): 81–8.
PubMed Abstract | Publisher Full Text

64. Estepa A, Frías D, Coll JM: ***In vitro* susceptibility of rainbow trout fin cells to viral haemorrhagic septicaemia virus.** *Dis Aquat Organ.* 1993; **15**: 35–9.
Publisher Full Text

65. Diago ML, Estepa A, López-Fierro P, *et al.*: **The *in vitro* infection of the hematopoietic stroma of trout kidney by hemorrhagic septicemia rhabdovirus.** *Viral Immunol.* 1993; **6**(3): 185–91.
PubMed Abstract | Publisher Full Text

66. Pham PH, Lumsden JS, Tafalla C, *et al.*: **Differential effects of viral hemorrhagic septicaemia virus (VHSV) genotypes IVa and IVb on gill epithelial and spleen macrophage cell lines from rainbow trout (*Oncorhynchus mykiss*).** *Fish Shellfish Immunol.* 2013; **34**(2): 632–40.
PubMed Abstract | Publisher Full Text

67. Wang W, Asim M, Yi L, *et al.*: **Abortive infection of snakehead fish vesiculovirus in ZF4 cells was associated with the RLRs pathway activation by viral replicative intermediates.** *Int J Mol Sci.* 2015; **16**(3): 6235–50.
PubMed Abstract | Publisher Full Text | Free Full Text

68. Pfefferkorn C, Kallfass C, Lienenklaus S, *et al.*: **Abortively Infected Astrocytes Appear To Represent the Main Source of Interferon Beta in the Virus-Infected Brain.** *J Virol.* 2016; **90**(4): 2031–8.
PubMed Abstract | Publisher Full Text | Free Full Text

69. Makris S, Bajorek M, Culley FJ, *et al.*: **Alveolar Macrophages Can Control Respiratory Syncytial Virus Infection in the Absence of Type I Interferons.** *J Innate Immun.* 2016; **8**(5): 452–63.
PubMed Abstract | Publisher Full Text | Free Full Text

70. Tafalla C, Sanchez E, Lorenzen N, *et al.*: **Effects of viral hemorrhagic septicemia virus (VHSV) on the rainbow trout (*Oncorhynchus mykiss*) monocyte cell line RTS-11.** *Mol Immunol.* 2008; **45**(5): 1439–48.
PubMed Abstract | Publisher Full Text

71. Ivashkiv LB, Donlin LT: **Regulation of type I interferon responses.** *Nat Rev Immunol.* 2014; **14**(1): 36–49.
PubMed Abstract | Publisher Full Text | Free Full Text

72. Alvarez-Torres D, Garcia-Rosado E, Fernandez-Trujillo MA, *et al.*: **Antiviral specificity of the *Solea senegalensis* Mx protein constitutively expressed in CHSE-214 cells.** *Mar Biotechnol (NY).* 2013; **15**(2): 125–32.
PubMed Abstract | Publisher Full Text

73. Collet B, Boudinot P, Benmansour A, *et al.*: **An Mx1 promoter-reporter system to study interferon pathways in rainbow trout.** *Dev Comp Immunol.* 2004; **28**(7–8): 793–801.
PubMed Abstract | Publisher Full Text

74. Kim MS, Kim KH: **Effects of NV gene knock-out recombinant viral hemorrhagic septicemia virus (VHSV) on Mx gene expression in *Epithelioma papulosum cyprini* (EPC) cells and olive flounder (*Paralichthys olivaceus*).** *Fish Shellfish Immunol.* 2012; **32**(3): 459–63.
PubMed Abstract | Publisher Full Text

75. Chinchilla B, Encinas P, Estepa A, *et al.*: **Transcriptome analysis of rainbow trout in response to non-virion (NV) protein of viral haemorrhagic septicaemia virus (VHSV).** *Appl Microbiol Biotechnol.* 2015; **99**(4): 1827–43.
PubMed Abstract | Publisher Full Text

76. Ke Q, Weaver W, Pore A, *et al.*: **Role of Viral Hemorrhagic Septicemia Virus Matrix (M) Protein in Suppressing Host Transcription.** *J Virol.* 2017; **91**(19): pii: e00279-17.
PubMed Abstract | Publisher Full Text | Free Full Text

77. Fierro-Castro C, Barrioluengo L, López-Fierro P, *et al.*: **Fish cell cultures as *in vitro* models of pro-inflammatory responses elicited by immunostimulants.** *Fish Shellfish Immunol.* 2012; **33**(2): 389–400.
PubMed Abstract | Publisher Full Text

78. Fierro-Castro C, Barrioluengo L, López-Fierro P, *et al.*: **Fish cell cultures as *in vitro* models of inflammatory responses elicited by immunostimulants. Expression of regulatory genes of the innate immune response.** *Fish Shellfish Immunol.* 2013; **35**(3): 979–87.
PubMed Abstract | Publisher Full Text

79. Anthony SM, Howard ME, Hailemichael Y, *et al.*: **Soluble interleukin-15 complexes are generated *in vivo* by type I interferon dependent and independent pathways.** *PLoS One.* 2015; **10**(3): e0120274.
PubMed Abstract | Publisher Full Text | Free Full Text

80. Boudinot P, Massin P, Blanco M, *et al.*: ***vig-1*, a new fish gene induced by the rhabdovirus glycoprotein, has a virus-induced homologue in humans and shares conserved motifs with the MoaA family.** *J Virol.* 1999; **73**(3): 1846–52.
PubMed Abstract | Free Full Text

81. Konig R, Zhou Y, Elleder D, *et al.*: **Global analysis of host-pathogen interactions that regulate early-stage HIV-1 replication.** *Cell.* 2008; **135**(1): 49–60.
PubMed Abstract | Publisher Full Text | Free Full Text

82. Paz S, Lu ML, Takata H, *et al.*: **SRSF1 RNA Recognition Motifs Are Strong Inhibitors of HIV-1 Replication.** *J Virol.* 2015; **89**(12): 6275–86.
PubMed Abstract | Publisher Full Text | Free Full Text

83. Hadian K, Vincendeau M, Mausbacher N, *et al.*: **Identification of a heterogeneous nuclear ribonucleoprotein-recognition region in the HIV Rev protein.** *J Biol Chem.* 2009; **284**(48): 33384–91.
PubMed Abstract | Publisher Full Text | Free Full Text

84. Ow SY, Salim M, Noirel J, *et al.*: **Minimising iTRAQ ratio compression through understanding LC-MS elution dependence and high-resolution HILIC fractionation.** *Proteomics.* 2011; **11**(11): 2341–6.
PubMed Abstract | Publisher Full Text

85. Schneider RJ, Mohr I: **Translation initiation and viral tricks.** *Trends Biochem Sci.* 2003; **28**(3): 130–6.
PubMed Abstract | Publisher Full Text

86. Connor JH, Lyles DS: **Inhibition of host and viral translation during vesicular stomatitis virus infection. eIF2 is responsible for the inhibition of viral but not host translation.** *J Biol Chem.* 2005; **280**(14): 13512–9.
PubMed Abstract | Publisher Full Text

87. Morgan MJ, Liu ZG: **Crosstalk of reactive oxygen species and NF-κB signaling.** *Cell Res.* 2011; **21**(1): 103–15.
PubMed Abstract | Publisher Full Text | Free Full Text

88. Gullberg RC, Jordan SJ, Moon SL, *et al.*: **Oxidative stress influences positive strand RNA virus genome synthesis and capping.** *Virology.* 2015; **475**: 219–29.
PubMed Abstract | Publisher Full Text | Free Full Text

89. Yurochko AD, Kowalik TF, Huong SM, *et al.*: **Human cytomegalovirus upregulates NF-kappa B activity by transactivating the NF-kappa B p105/p50 and p65 promoters.** *J Virol.* 1995; **69**(9): 5391–400.
PubMed Abstract | Free Full Text

90. Shao J, Huang J, Guo Y, *et al.*: **Up-regulation of nuclear factor E2-related factor 2 (Nrf2) represses the replication of SVCV.** *Fish Shellfish Immunol.* 2016; **58**: 474–82.
PubMed Abstract | Publisher Full Text

91. Raida MK, Buchmann K: **Temperature-dependent expression of immune-relevant genes in rainbow trout following *Yersinia ruckeri* vaccination.** *Dis Aquat Organ.* 2007; **77**(1): 41–52.
PubMed Abstract | Publisher Full Text

92. Ortega-Villaizan M, Chico V, Martinez-Lopez A, *et al.*: ***In vitro* analysis of the factors contributing to the antiviral state induced by a plasmid encoding the viral haemorrhagic septicaemia virus glycoprotein G in transfected trout cells.** *Vaccine.* 2011; **29**(4): 737–43.
PubMed Abstract | Publisher Full Text

93. Nombela I, Puente-Marin S, Chico V, *et al.*: **Dataset 1 in: Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication.** *F1000Research.* 2017.
Data Source

94. Nombela I, Puente-Marin S, Chico V, *et al.*: **Dataset 2 in: Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication.** *F1000Research.* 2017.
Data Source

95. Nombela I, Puente-Marin S, Chico V, *et al.*: **Dataset 3 in: Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication.** *F1000Research.* 2017.
Data Source

96. Nombela I, Puente-Marin S, Chico V, *et al.*: **Dataset 4 in: Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication.** *F1000Research.* 2017.
Data Source

97. Nombela I, Puente-Marin S, Chico V, *et al.*: **Dataset 5 in: Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication.** *F1000Research.* 2017.
Data Source

98. Nombela I, Puente-Marin S, Chico V, *et al.*: **Dataset 6 in: Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication.** *F1000Research.* 2017.
Data Source

99. Nombela I, Puente-Marin S, Chico V, *et al.*: **Dataset 7 in: Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication.** *F1000Research.* 2017.
Data Source

Open Peer Review

Current Referee Status: ? ?

Version 1

Referee Report 30 November 2017

doi:10.5256/f1000research.14081.r27745

? **Johannes M. Dijkstra**
Institute for Comprehensive Medical Science, Fujita Health University, Toyoake, Japan

Nombela et al. describe in what they claim to be defense mechanisms in trout red blood cells in response to halted replication of VHSV virus.

Major comments:

The study suffers from the effort to simultaneously answer a few unknowns. Can VHSV infect trout erythrocytes? Does infection by, or exposure to, VHSV virus modify the expression of genes with an anti-virus function? Do those altered gene expression levels have a measurable immune effect (which in this article is measured by the effect on cell line TSS)?

In my opinion, the authors show understanding of the complexity of those questions, but do not take sufficiently control of them. I am not satisfied with any of the story lines. My main concerns are that it is unclear for many of the presented data (i) whether the enhanced expression of immune molecules are due to RBC infection or due to other stimulations of the RBCs by the virus preparation, (ii) whether the changes in immune molecule expression are due to stimulation by virus preparation or due to time of culturing, and (iii) whether the expression levels of immune molecules reach meaningful levels or are just variation within what could be considered as “non-functional background levels”.

At the very positive side, the authors addressed an important question, and delivered an honest and elaborate piece of work. Therefore, I will not reject the paper, but I do request the addition of experimental data that in my opinion are necessary for better interpretation of the currently presented data in relation to actual VHS disease.

The authors should infect rainbow trout cells which they deem (sufficiently representative of) the natural host cells of VHSV, and use the UV-inactivated supernatant for stimulation of trout RBCs and compare the effect on RBC immune molecule expression with the effect after RBC incubation with VHSV. Alternatively, they can use inactivated serum of VHSV-infected trout. My guess is that the released cytokines have a much stronger effect on those erythrocytes than the viruses to which the erythrocytes are hardly receptive.

The authors should also use those supernatants of natural host cells, or sera from infected trout, for stimulation of TSS cells, and compare the effects quantitatively with those after stimulation with the supernatant of VHSV-exposed erythrocytes.

The above requested set of experiments (or modifications thereof, depending on the preferences of the authors) should help to quantitatively estimate the direct effect of VHSV on erythrocytes, and the effect of VHSV-stimulated erythrocytes on other cells, in comparison with other routes of immune stimulation during VHSV infection.

Detailed comments:

Why did the authors use an MOI of 1? Even if such MOI is achieved, only half of the cells are expected to be infected. In this case the actual MOI for red blood cells probably was far below 1, because the MOI was calculated based on infection of the receptive EPC cells.

How were the viruses prepared? It seems that they were generated on EPC cells, but the details are important. Namely, other than the viruses, the infected cells also release cytokines which may have a cross-species effect.

The only presented data that I find convincing for that red blood cells were infected were the experiments shown in Fig. 1E and Fig. 1F, namely after pretreatment with neuraminidase (Fig. 1E) and infection with an MOI=100 (Fig. 1G; even in that case only 1/6 cells shows infection). However, none of the experiments on immune molecule expression was done under those conditions.

In the experiments, expression levels are compared with those of “control cells”. In some cases those control cells are not specified, while in other cases they are said to be the T=0 cells. However, this does not take into account that also the time of culture can have a significant effect on gene and protein expression levels. Most of the expression level effects reported in this article are quite small (e.g. from very low to only two-fold higher), and a possible “culture-time effect” should have been excluded.

The introduction should give detailed descriptions of what is known or unknown (i) about natural target cells and receptors used by VHSV for infection, and (ii) about fish erythrocytes and to what extent they have a normal metabolism. The introduction should also give an indication of the abundance of erythrocytes, which is relevant because many small amounts of cytokine could make a big amount, and also because any “intelligent” virus will do its best to avoid interaction with this abundant and for the virus non-productive cell type.

In the title, shouldn’t it be “in response to halted replication of VHS virus.”?

In the abstract and in the text: “after 6 hours postexposure” is double.

In the abstract, in the sentence “Co-culture assays of RBCs with TSS”, it should be made clear that those RBCs were stimulated with UV-inactivated VHSV.

In the introduction, a number of speculations are presented as facts:

- Fish poikilothermic nature results in a delayed antigen affinity maturation, memory and lymphocyte proliferation.
- Fish have unique phagocytic B lymphocytes. (later than the reference, also mammalian B cells with phagocytic ability have been found)
- Fish have stronger innate immune responses.
- To compensate for those immune deficiencies, fish have unique phagocytic B lymphocytes and stronger innate immune responses.

I don't understand the "Thus" in the sentence "Thus, fish RBCs generate a wide variety of immune-related gene transcripts when viruses highly replicate inside them".

In Fig. 1A, how was the PCR value for N gene determined at T=0? Was that before or after addition of the viruses, and could the difference between T=0 and the other time points be explained by amplification from RNA in virions?

Fig. 1B seems to argue against the assumption that the RNAs amplified in Fig. 1A were derived from an infection (see also my previous point). In addition, although the relative comparison between the RTG2 and RBC results as presented in Fig. 1B should be OK, it is unclear to me from the materials and methods section how the absolute quantitative statement "However, a ratio of 2 was observed in RBCs, compared to the ratio of 8 found in RTG-2 cells, at 1 and 3 hpe (Figure 1B)" can be made.

I am not convinced that Fig. 1D is evidence for replication between days 3 and 6, since the titer goes down >5000-fold from day 0 to day 3, and then stays very low. The authors should make clearer whether they feel that the small increase in virus titer between days 3 and 6 is only suggestive of virus replication, or that such replication is supported by proper statistics.
As for the NH4Cl effect observed in Fig. 1D. Can a chemical effect of NH4CL on the integrity of virions stuck to the outside of RBCs be excluded from explaining the results? Furthermore, I would like the authors to elaborate, possibly in the introduction section, on endocytosis in regard to erythrocytes and VHSV infection. Could it be that only immature erythrocytes are expected to display efficient endocytosis, and might the Fig. 1F result be explained by differences in erythrocyte subpopulations?

I don't understand the sentence "As a result, the VHSV RNA inside RBCs was increased about ten times at 3 hpe", because the increase seems to be from around 0.6 to 3.4, which is closer to a six-fold increase.

For discussion of the Fig. 1F result, the authors should explain the intracellular organization of RBCs (which are unusual cells), and where VHSV is expected. The sentence "along the cytoplasm and nucleus" can't be understood, and gives the impression that the authors do not know where to expect (normal) cytoplasm in RBCs. Although they observe "along the nucleus", which I think is the correct observation, the authors discuss the possibility of N protein being present in the nucleus. It is not wrong to present that as a possibility to partially explain their observations, but the authors should declare clearer that their observations do not necessitate that N protein is present in the nucleus. To superficial readers it now looks as if they claim detection of N protein in the RBC nucleus.

In Fig. 3 legend, the B and C order should be altered.

(writing error) were co-culture with > were co-cultured with

In the Transwell system, the authors tried to get rid of RBC-attached virions with a single non-stringent wash. I doubt that such was sufficient for complete removal, and in the following 24 hours of co-incubation some virions or viral products may have diffused to the TSS cells.

As for Fig. 4. Is it OK to assume linear regression based on only two time points? Wouldn't it be more proper to indicate all individual observations with dots? What is a 0-fold increase? In Figs. 4A and 4C, all three lines need explanation.

I can't trust the claims based on Fig. 8. In Fig. 8A, why were protein amounts loaded in the Control and

VHSV lanes so different? I don't believe that densiometry analysis technique for Western blot bands is sufficiently sensitive, especially not if comparing different ranges of band densities, to reliably claim an about 15% difference as done in Fig. 8B. In addition, for densiometry analysis, the Fig. 8A Actin blot is a horrible result because only half of the lane was properly exposed to the Western treatment. If the Fig. 8A result truly is a "representative" result, as claimed by the authors, the Fig. 8 based conclusions can't be taken seriously.

Trout erythrocytes are known to express MHC class I (Dijkstra *et al.* (2003)[1]; Sarder *et al*. (2003)[2]). Because MHC class I is a molecule upregulated during virus infection, it would be interesting to see the effect on its expression in RBCs by exposure to VHSV. Likewise, and especially because Nombela et al. discuss the proteasome, it would be interesting to see the regulation of the genes for the immuno-proteasome specific subunits.

References

1. Dijkstra J, Köllner B, Aoyagi K, Sawamoto Y, Kuroda A, Ototake M, Nakanishi T, Fischer U: The rainbow trout classical MHC class I molecule Onmy-UBA*501 is expressed in similar cell types as mammalian classical MHC class I molecules. *Fish & Shellfish Immunology*. 2003; **14** (1): 1-23 Publisher Full Text

2. Sarder MR, Fischer U, Dijkstra JM, Kiryu I, Yoshiura Y, Azuma T, Köllner B, Ototake M: The MHC class I linkage group is a major determinant in the in vivo rejection of allogeneic erythrocytes in rainbow trout (Oncorhynchus mykiss).*Immunogenetics*. 2003; **55** (5): 315-24 PubMed Abstract | Publisher Full Text

Is the work clearly and accurately presented and does it cite the current literature?
Partly

Is the study design appropriate and is the work technically sound?
No

Are sufficient details of methods and analysis provided to allow replication by others?
No

If applicable, is the statistical analysis and its interpretation appropriate?
Partly

Are all the source data underlying the results available to ensure full reproducibility?
Partly

Are the conclusions drawn adequately supported by the results?
Partly

Competing Interests: No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Referee Report 27 November 2017

doi:10.5256/f1000research.14081.r27680

Aleksei Krasnov
Nofima AS, Ås, Norway

The paper reports studies with red blood cells (RBC) of rainbow trout infected with Viral Haemorrhagic Septicaemia virus (VHSV). RBC most likely do not support propagation of VHSV and immune responses to the pathogen were small by magnitude. Still, experiments and analyses were well designed and implemented, applied diverse methods and therefore publication will be useful and interesting for experts in the area.

Major comment
Suppression of innate antiviral immunity in infected RBC is included in the abstract as one of the key findings. However, of several genes analysed with qPCR only ifn1 showed down-regulation and only at one time-point. Other genes exhibited at best a slight tendency and differences from control were small. Reference to high variation is not convincing and does not overcome the lack of significance. Delete sentence “It is noteworthy to highlight the elevated inter-individual variability found in trout RBCs immune response, for most of the proteins and genes assayed, which could prevent to obtain statistical significance in most of the cases although regulations were apparent” (pages 9-10), this statement is trivial. M&M do not tell if each RBC culture was from an individual animal. If not, then variation was technical by character suggesting problems with methods. I also suggest to delete or at least shorten discussion of viral suppression of IFN-dependent responses in fish (page 16, 1st paragraph). I would emphasize strong induction of ROS scavengers as most impressive result of this study.

Specific comments

- Figure 2. Indicate method in the legend – qPCR? Change label of Y-axis: fold instead of fold of increase.
- Figure 4. The number of replicates (n = 6) is too small for regression and correlation analyses. I strongly suggest to plot empirical data, trend lines alone are not convincing. Judging from the figures, ifn1 levels were in the range from 0 to 15. Units should be explained. Furthermore, it is unclear how such differences was achieved taking into account minor responses of ifn1 to IHNV in trout RBC.
- Figure 10. Explain grey and black bars in the legend.
- Page 16. Delete paragraph “It is noticeable that the iTRAQ-based protein…” – no need to explain that proteomic analyses fail to detect low abundance proteins including cytokines.
- Page 17, 1st paragraph. NFkB can be mentioned but extensive discussion is not warranted since study did not produce any experimental data for this gene or protein.
- “It is evident that the antiviral response of RBCs is low compared to other cells of the immune system” – this statement is wrong. Virus infected fish RBC develop immune responses of huge magnitude. “Inter-individual variability” – if RBC cultures represented individuals, this must be explicitly stated in M&M (see comment above). Given small number of replicates, discussion of high and low responders is not supported with data.

Is the work clearly and accurately presented and does it cite the current literature?

Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Partly

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
No source data required

Are the conclusions drawn adequately supported by the results?
Partly

Competing Interests: No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.