pathogen and the disease kinetics, little is known about the molecular mechanisms underlying resistance to this disease.
Within the context of the European H2020 project Vivaldi, an experimental population of Manila clam families was produced, and a batch of juvenile individuals from this population were subjected to a 28-day controlled challenge with *Vibrio tapetis* strain CECT4600. Dual diagnosis was carried out to distinguish between healthy and diseased individuals post-challenge: shells were visually diagnosed for presence of BRD, and a PCR method was adapted to detect *V. tapetis* DNA. Total protein extractions were carried out using whole-body tissue homogenates of healthy and diseased clams and proteins were identified using LC-MS/MS. 2093 protein sequences were matched against a reference transcriptome of the Manila clam, and protein intensities based on label-free quantification were compared to reveal 32 and 55 significant proteins in healthy and diseased clams, respectively. These results provide us with important information regarding the major cell processes and the roles they may play in the resistance of *R. philippinarum* to BRD.
Keywords: *Ruditapes philippinarum*, Brown Ring disease, proteomics, disease resistance, aquaculture

Corresponding author.
E-mail addresses: morgan.smits@phd.unipd.it, morgan.smits@univ-brest.fr (M. Smits).

O-126.

Insights into the microbiota of farmed and wild Mytilus SP: Is there a link between bacteria communities and host susceptibility?

Yosra Ben Cheikh [1,#], Marie Agnès Travers [2], Frank Le Foll [1], Nathalie Giusti [1].

[1] University of Le Havre Normandy, Environmental Stress and Aquatic Biomonitoring, UMR-I 02 SEBIO, 25 rue Philippe Lebon, F-76063, Le Havre, France
[2] Ifremer, SG2M-LGPMM, Laboratoire de Génétique et Pathologie des Mollusques Marins Avenue de Mus de Loup, 17390, La Tremblade, France

Abstract
Since 2014, Mytilus species are affected by mass mortality outbreaks especially in French shellfish farms. A first investigation demonstrated the potential implication of *Vibrio splendidus* through the evidence of a virulent strain10/068 1T1 able to colonize the blue mussel by bypassing external defense barriers and impairing hemocyte activities .
In this study, we explore the role of microbiota in host susceptibility to microbial disease. Different Mytilus species (M. edulis, M. galloprovincialis and hybrid *M. edulis*/*M. galloprovincialis*) were sampled from mussel farms impacted by seasonal mortalities and from natural site. Then, we explored 1) the composition of bacterial microbiota, 2) the mussel susceptibility to the pathogen *V. splendidus* 10/068 1T1 and 3) the impact of Vibrio infection on microbiota bacteria communities.
Keywords: Mytilus sp, microbiota, *V. splendidus*, Vibrio infection

Corresponding author.
E-mail address: yosra.ben-cheikh@univ-lehavre.fr (Y. Ben Cheikh).

O-127.

Gene encoding enzymes in the urea cycle and polyamine synthesis are modulated during an inflammatory response in rainbow trout (*Oncorhynchus mykiss*)

T. Clark [1], J. Tinsley [2], D.J.Macqueen [1,3], S.A.M. Martin [1,#].

[1] School of Biological Sciences, University of Aberdeen, Aberdeen, AB24 2TZ
[2] BioMar Ltd, Grangemouth Docks, Grangemouth, FK3 8UL, UK
[3] Current address: The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, EH25 9RG, UK

Abstract
The urea cycle and the genes encoding the major enzymes is still poorly characterised in teleost fish and to date there is no information as to how these genes are regulated during inflammation. Central to the urea cycle is the metabolism of arginine and its precursor amino acids, ornithine and citrulline. In salmonids, arginine is an essential amino acid as sufficient quantities cannot be synthesised endogenously and must be obtained in the diet. Arginine has roles in both the inflammatory innate immune response and subsequent tissue healing. To further understand the role of the urea cycle and related cycles (polyamine synthesis and nitric oxide production) in teleosts, we characterised gene families encoding the key enzymes in this pathway, their expression during an inflammatory response and changes in the free amino acid levels in the blood plasma following *Aeromonas salmonicida* challenge. Due to two whole genome duplication events in salmonid evolutionary history, several genes in these pathways have paralogous copies, with divergent expression patterns. The modulation of the genes involved in the urea cycle during inflammation could open up new lines of research for both fish health and nutrition.
Keywords: Urea cycle, Polyamines, Arginine, Inflammation, Functional feeds

Corresponding author.
E-mail address: sam.martin@abdn.ac.uk (S.A.M. Martin).

O-128.

Effect of different stressors on the expression of glucocorticoid receptor 1 (GR1) and GR2 and their implications in the transcriptional immune response in mucosal surfaces

Eva Vallejos-Vidal [1], Beatriz Sanz Milián [1], Sara Urquizu [1], Aleix Castellvi [1], Irene Brandts Busom [1], Mariana Teles [1], Juan Miguel Mancera [2], Lluis Tort [1], Felipe E. Reyes-López [1,#].

[1] Department of Cell Biology, Physiology and Immunology, Universitat Autònoma deBarcelona, 08193, Bellaterra, Spain
[2] Departamento de Biología, Universidad de Cádiz, Spain

Abstract
Cortisol is considered the most common physiological indicator of stress in fish. It plays a role regulating energy homeostasis, osmotic balance maintenance, and metabolic reorganization. As a consequence, cortisol may compromise the normal function of other biological processes including the host defense through a delay or reduction of the immune response. Its mechanism of action is mediated through glucocorticoid receptors (GRs) in responsive cells. In Perciformes like sea bass (*Dicentrarchus labrax*), two receptors, GR1 and GR2 have been described, but in gilthead sea bream (*Sparus aurata*) there is still little information about them. Thus, the aim of this study was to deep into the characterization of GR sequences of seabream and their expression under chronic and acute stress. For this purpose, sea bream were subjected to a high-intensity chronic stress for 40 days and the sequences for GR1 and GR2 were identified by RT-PCR and sequencing. In agreement with previous data in other Perciformes species, a deletion/insertion in the C domain (DNA-binding region) between GR1 and GR2 was found in the nucleotide sequence. Since there are previous antecedents in fish that GR1 and GR2 respond to different cortisol concentration levels, we also aimed to evaluate whether different stressors (in terms of intensity and duration) may differentially modulate their gene expression. To do it, gilthead sea bream were subjected to an acute stressor (1 min air exposure) monitored at 1, 6 and 24 hours post-stress and to a long-term stressor (two crowding stress conditions: 40 and 70 kg/m3) and their response evaluated at 7 and 14 days post-stress. The implications of the stress response upon the GR1 and GR2 expression and their consequences on the expression of immune-related genes was assessed. A differential expression of GR1 and GR2 under the different stress situations was observed, confirming the presence of