Gill lesions are the main cause of death in yellowfin seabream (Acanthopagrus latus) following infection with Amyloodinium ocellatum

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Amyloodiniosis, caused by the ectoparasite Amyloodinium ocellatum, affects the healthy development of mariculture. This study used a local infection method to identify the pathogenic target organ responsible for the death of infected fish. Comparing the relationship between the abundance of trophonts in gills and skin with the mortality of infected fish using local infection showed that severe gill infections cause the mortality of infected fish.

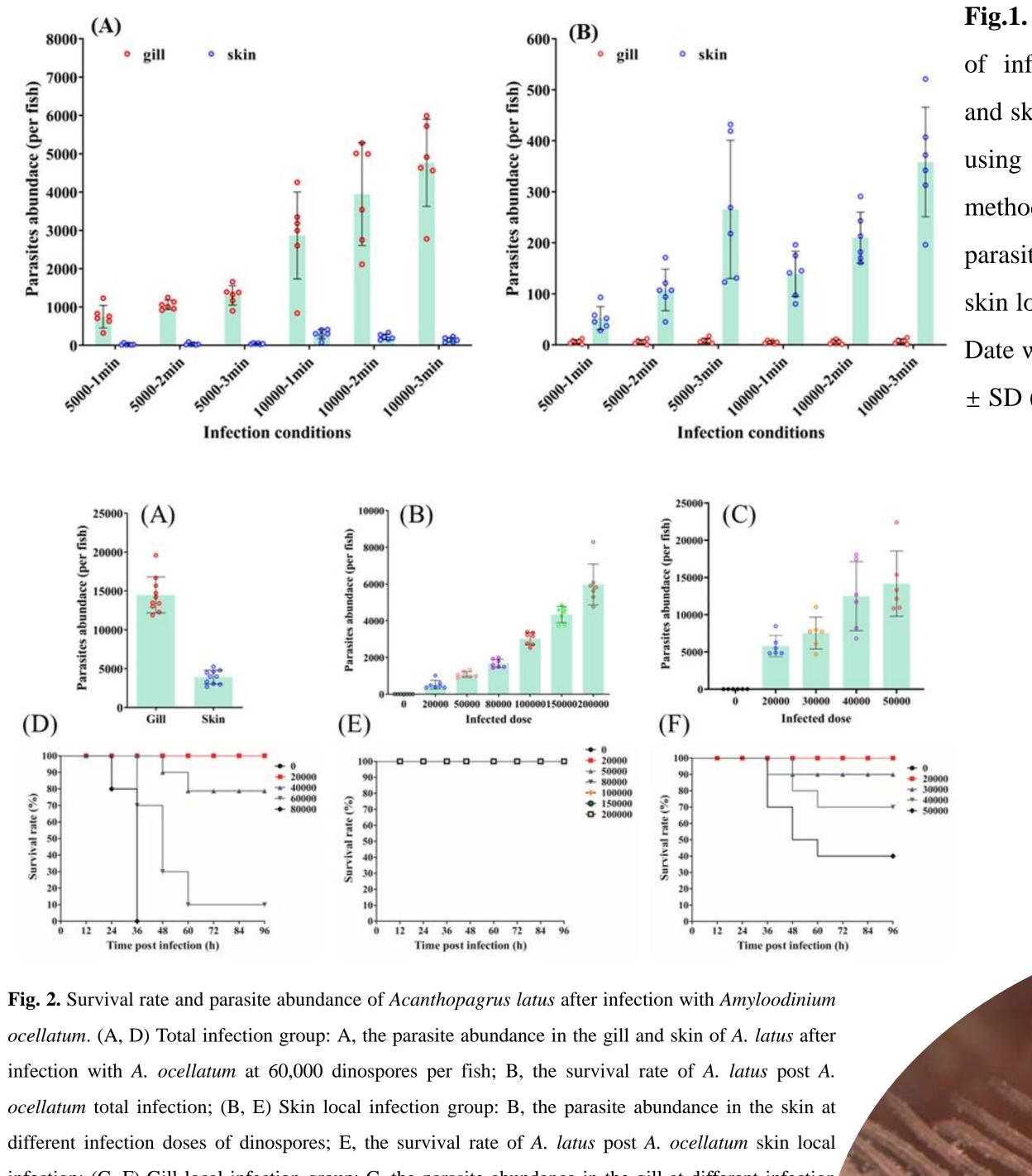


Fig.1. Parasite abundance of infected fish. (A) Gill and skin parasite abundance using gill local infection methods; (B) Gill and skin parasite abundance using skin local infection methods. Date was presented as mean \pm SD (n= 6).

> Fig. 3. Trophonts parasitizing on gills, fins and skin after infection with Amyloodinium ocellatum. For skin infections, trophonts were parasitized on the scales of infected fish. Fig. 4. Diameter of trophonts parasitizing

> > mean \pm SD (n= 20).

on different organs. Date was presented as Diameter Gill Skin

infection; (C, F) Gill local infection group: C, the parasite abundance in the gill at different infection doses of dinospores; F, the survival rate of A. latus post A. ocellatum gill local infection. Histopathology **MEGRE**

Fig. 6. TUNEL staining of gill in control group and infection group. Both normal and apoptotic cells nuclei can be stained with blue fluorescence, and only apoptotic cells

DNA can be stained with red fluorescence. (E)

Histological pathological changes in the gill and skin of Acanthopagrus latus with HE-stained sections. (A) The gill of the control fish: well-arranged filaments and tightly packed epithelial cells; (B-G) The gill the A.ocellatum infected fish: structurally disordered, epithelial cell degeneration and hyperplasia leading to fusion adjacent lamellae (red circle), detachment of the epithelium lamellar disappearance of the secondary lamellae (red arrow), inflammatory foci with lymphocytic massive infiltration (white circle); (H) The different layer skin the control fish; (I) The different layer skin of the A.ocellatum

infected fish.

Fig. 8. Species-level variation of Acanthopagrus latus gill and skin microbiota present in infected and control groups. Circles radiating outwards from the figure represent the taxonomic level from phylum to genus, each small circle at a different taxonomic leve(A) represents a taxon at that level, and the size of the diameter of the small circle represents the size of the relative abundance. Species with no significant differences are colored yellow, biomarkers with significant differences are coloured according to the

IN-S C-S IN-G Verrucomicrobiota Bacteroidota p Bacteroidota p_Firmicutes p_unclassified Firmicutes Desulfobacterota Verrucomicrobiota unclassified elati. Fusobacteriota

Microbial community

Fig. 7. The OTU distribution and mean relative abundance of bacterial community. (A) Venn diagram of skin microbiota OTU distribution; (B) Venn diagram of gill microbiota OTU distribution; (C) Relative abundance at the phylum level for infected group and control group skin; (D) Relative abundance at the phylum level

 h: f Crocinitomicaceae i: o_Flavobacteriales k: c_Verrucomicrobiae l: o_Verrucomicrobiales m: f_Rubritaleaceae n: g_Rubritalea o: s_norank_g_Rubritalea p: g_norank_f_Spirosomace. q: s_norank_f_Spirosomace r: f_Spirosomaceae s: o_Cytophagales t: s_Bacteroides_vulgatus o IN S o C S

(A)

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for infected group and control group gill. a0: g_Staphylococcus g: s_norank_f_Crocinitomicaceae al: s Staphylococcus capitis a2: g_Klebsiella a3: s_Klebsiella_pneumoniae a4: g_Haemophilus a5: s_Haemophilus_parainfluenz a6: f_Pasteurellaceae a7: f Ruminococcacea a8: f_Pseudomonadaceae a9: g_Pseudomonas b0: g_Veillonella b1: f Veillonellaceae b2: o Veillonellales-Selenomonadale

 b9: o Oscillospirale • c0: g_Escherichia-Shigella o cl: s Escherichia coli c2: g_norank_f_Flavobacteriaceae c3: s_norank_f_Flavobacteriaceae c4: s_Acinetobacter_baumannii c5: g_Acinetobacter c6: f_Moraxellaceae c7: g_norank_f_Chlamydiales_Incertae_Sedis c8: s Candidatus Parilichlamydia sp. RB230513-5
e8: s Sargassum vachellianum c9: f_Lactobacillaceae d0: f_Bacteroidaceae d1: g_Bacteroides d2: o Lachnospirales b3: s_Lactobacillus_salivarius d3: f Lachnospiraceae

a: g_Pelomonas b: s Pelomonas saccharophila c: s_Rhodococcus_fascians d: f_Nocardiaceae e: g_Rhodococcus f: s_norank_g_Clostridium_sensu_stricto h: o Clostridiales i: f_Clostridiaceae j: s_Methylobacterium_komagatae k: g_Renibacterium l: s_norank_g_Renibacterium m: g_Ruegeria n: s_Ruegeria_pomeroy o: o_Corynebacteriales p: f_Halomonadaceae a9: s_norank_f_Crocinitomicaceae q: g_Halomonas b0: f_Crocinitomicaceae

o r: s norank g Halomonas s: g_Phaeocystidibacter

t: s_norank_g_Phaeocystidibacte

u: f_Cryomorphaceae o v: g_norank_f_Rhodobacteraceae w: s_norank_f_Rhodobacteraceae x: g_Sediminibacterium y: s_norank_g_Sediminibacterium z: s_Flavobacterium_sp._CC-PY-35 a0: g_Flavobacterium al: o_Rhodobacterales a2: f_Rhodobacteraceae a3: c_Verrucomicrobiae a4: o_Verrucomicrobiale a5: f_Rubritaleaceae a6: g_Rubritalea a7: s_norank_g_Rubritalea a8: g_norank_f_Crocinitomicaceae

b1: g_Tenacibaculum

b3: f_Flavobacteriaceae

b2: s norank g Tenacibaculum

b7: g_Paracoccus b8: s_norank_g_Paracoccus b9: g_Incertae_Sedis © c0: s_norank_g_Incertae_Sedis c1: g_Pedomicrobium 6 c2: s_norank_g_Pedomicrobium 6 c3: g_Tropicibacter 6 c4: s_norank_g_Tropicibacter 6 c5: f_Erwiniaceae oc6: g_Pantoea e7: s_norank_g_Pantoea

b4: o_Flavobacteriales

b5: s_norank_g_Leuconostoc

b6: s_Streptococcus_pyogenes

o e0: o Pseudomonadales

e2: o_Enterobacterales

e4: s_norank_g_Prevotella_9

e7: c Gammaproteobacteria

 f0: g_norank_f_Saprospirace fl: f_Saprospiraceae

e3: g_Prevotella_9

e5: f_Prevotellaceae

o e9: p_Proteobacteria

• f2: o_Bacteroidales

6 f3: o_Chitinophagales

c6: p_Firmicutes

o el: c Clostridia

Acknowledgement

group annotation.