

Microbiota and histological alterations in cultured *Isostichopus badiionotus* juveniles affected by skin ulceration syndrome

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INTRODUCTION

 Skin Ulceration Syndrome (SUS) severely impacts sea cucumber aquaculture, causing progressive ulceration and high mortality^{1,2}

 Although linked to environmental stress and microbial dysbiosis, histological characterization of tissue damage is scarce^{1,3}

 The limited understanding of *I. badiionotus* microbiota has constrained progress in elucidating SUS pathogenesis.

OBJECTIVES

1 To characterize the intestinal and skin microbiota of *I. badiionotus* juveniles affected by SUS cultured in Yucatan, Mexico by 16s RNA sequence.

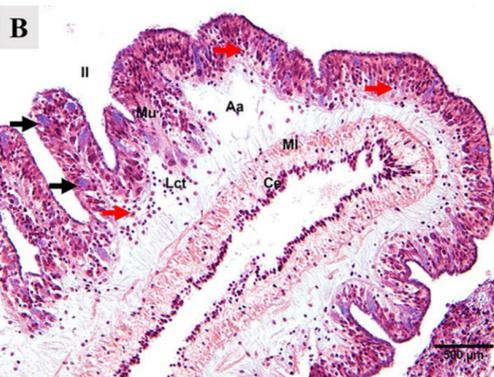
2 To determine the type and extension of tissue damage by histology using H&E stain.

RESULTS

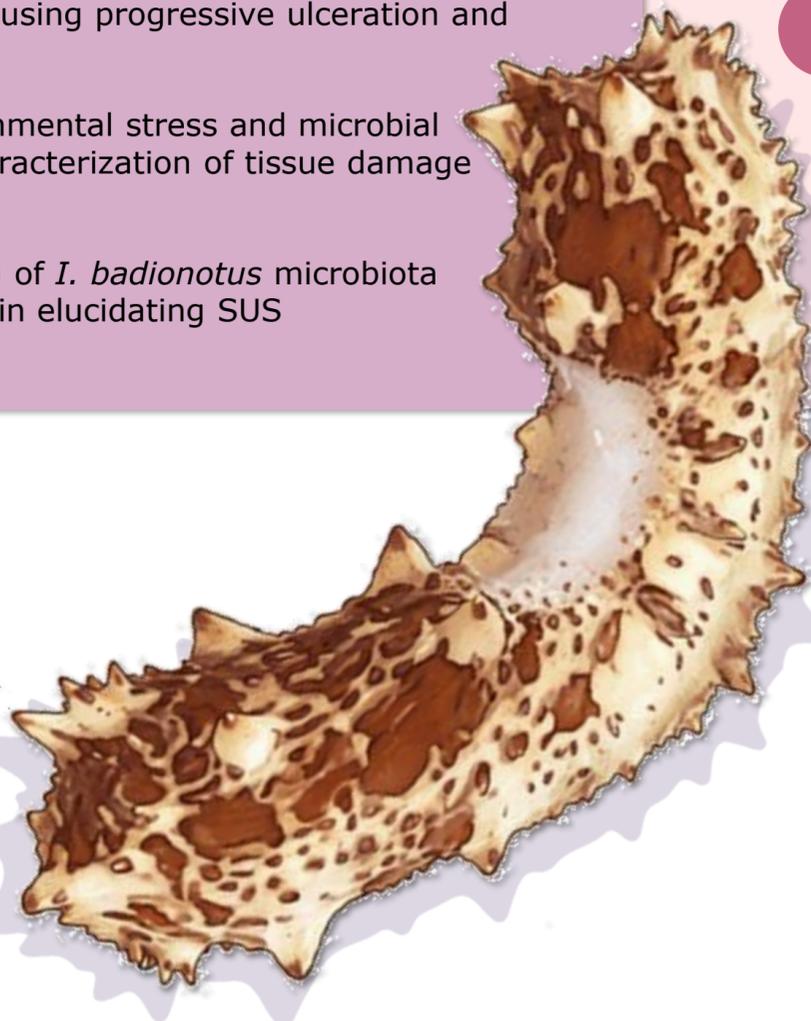
Histology analysis



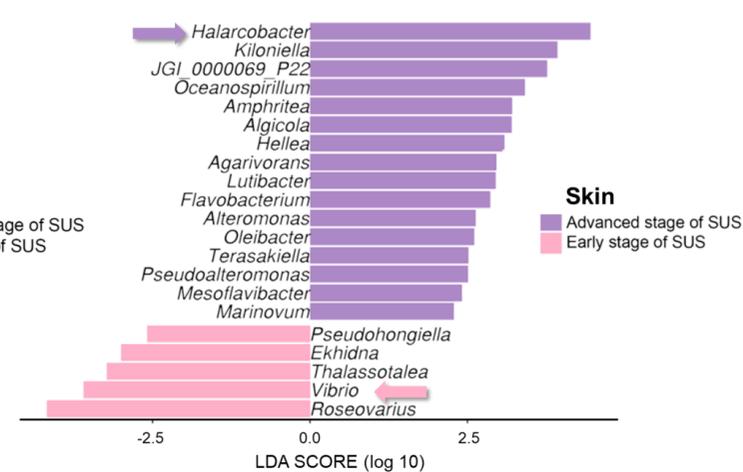
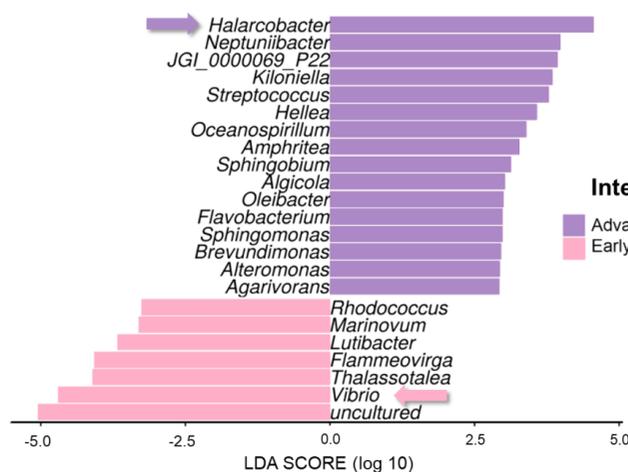
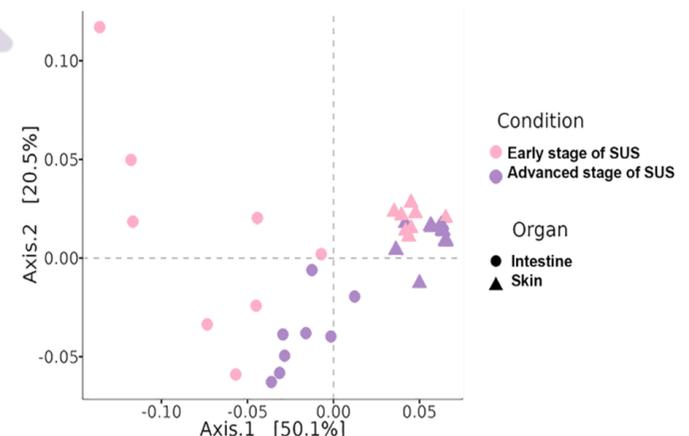
A. Histological cross-section of the posterior intestine of *I. badiionotus* juvenile with SUS in the early stage



B. Histological cross-section of the posterior intestine of *I. badiionotus* juvenile with SUS in the advanced stage



Molecular analysis



CONCLUSION

 Absence of visible lesions did not indicate health because juveniles were already in early SUS.

 Disease progression was marked by concurrent histological damage and shifts in microbial community structure.

 SUS in cultured juveniles was linked to intestinal dysbiosis rather than a single causative pathogen.

 Opposing trends in *Vibrio* and *Halarcobacter* (syn. *Arcobacter*) highlight their potential role as keystone genera in disease development.

REFERENCES

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