TRANSCRIPTOME-BASED IDENTIFICATION OF GROWTH-ASSOCIATED SNPS IN THE SANDFISH *HOLOTHURIA SCABRA*

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ABSTRACT

Growth is a critical trait influencing aquaculture productivity in the high-value tropical sea cucumber *Holothuria scabra*, yet the genetic basis underlying growth variation remains poorly understood. In this study, **transcriptome sequencing was performed on fast- and slow-growing juveniles to identify putative growth-associated single-nucleotide polymorphisms (SNPs)**. Reads were mapped against the reference genome assembly of Zhong et al. (2024), GenBank accession no. GCA_037179385.1 using STAR 2.7.0f. Variant calling with GATK v6.1.0 identified **4,035,955 variants**, which were subsequently filtered in PLINK v2.0, yielding **142,432 high-quality SNPs**. Among these, **98 SNPs were significantly associated with growth phenotype** following FDR-BY correction ($p \leqslant 0.05$). Variant effect prediction using SnpEff classified the significant SNPs as modifier, synonymous, missense, or stop/deletion variants. Functional annotation revealed associations with genes involved in **signal transduction, transcriptional regulation, RNA processing, metabolism, stress response, and several uncharacterized proteins that may serve as species-specific growth regulators**. These growth-associated SNPs represent promising molecular markers for selective breeding and genome-informed broodstock management. Thus, this **integrative transcriptomic approach** highlights the potential of genomics to enhance aquaculture productivity, improve breeding strategies, and support the sustainable production and genetic conservation of *Holothuria scabra.*

INTRODUCTION

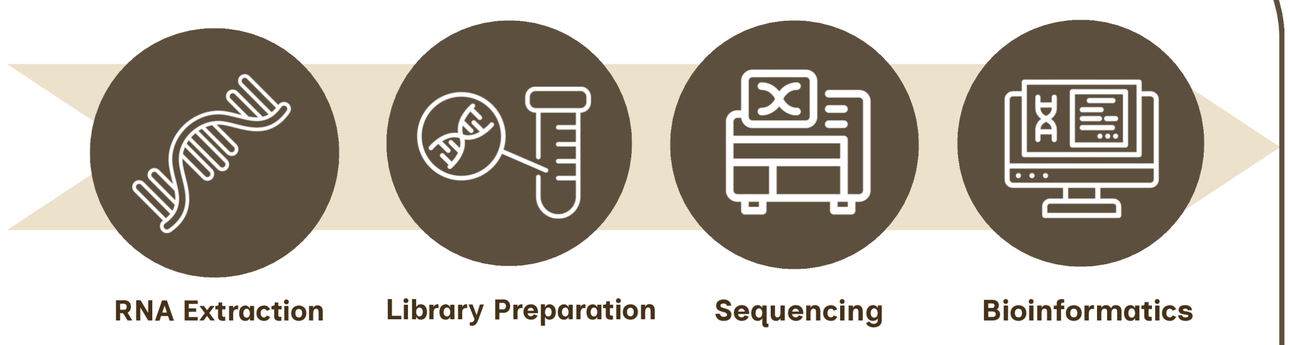
Sandfish (*Holothuria scabra*) as a high-value aquaculture species

Growth performance as a key trait in sustainable fisheries production

Need for identifying growth-associated single polymorphisms (SNPs) of *H. scabra*

Important for the development of genome-informed strategies for aquaculture

METHODOLOGY



Sampling Sites

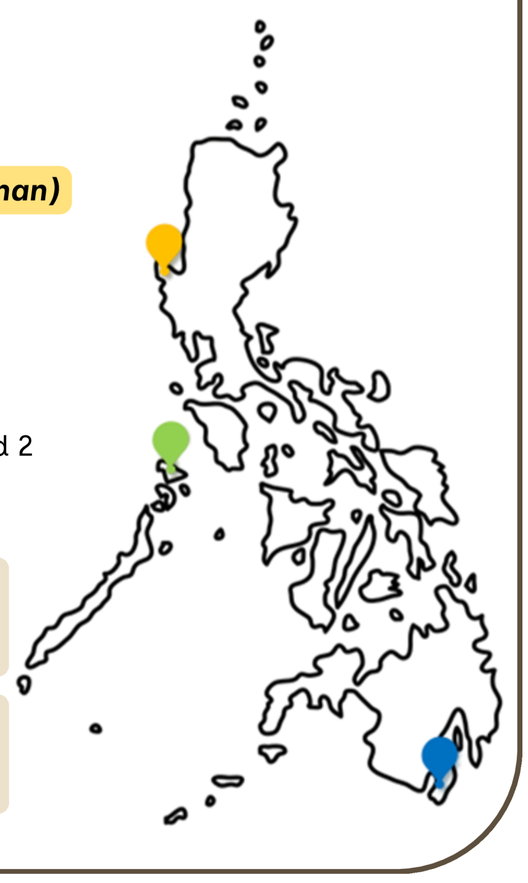
- ***Bolinao Marine Laboratory (Bolinao, Pangasinan)***
- ***Private hatchery (Coron, Palawan)***
- ***Private hatchery (Alabel, Sarangani)***

For each location, pooled samples were collected in duplicate per growth category, except in Bolinao where triplicate samples were collected (2 fast- and 2 slow-growth pools; 3 each in Bolinao).



Slow growing
8 pooled samples (40 individuals/pool)

Fast growing
8 pooled samples (7 individuals/pool)



RESULTS AND DISCUSSION

A reference-based approach to variant calling *was implemented using GenBank Accession GCA_037179385.1 (Zhong et al. 2024)*

4,035,955 *initial variants identified*

SNP filtering
80% call rate, 70% missingness, MAF<0.05, LD pruning

142,432 SNPs *after filtering*

Association analysis *using PLINK 2.0*

98 *out of 142,432 SNPs were associated with* ***GROWTH***



Functional annotation linked the identified SNPs to genes involved in **signal transduction, transcriptional regulation, RNA processing, metabolism, stress response, and potential species-specific growth regulation** in *H. scabra.*

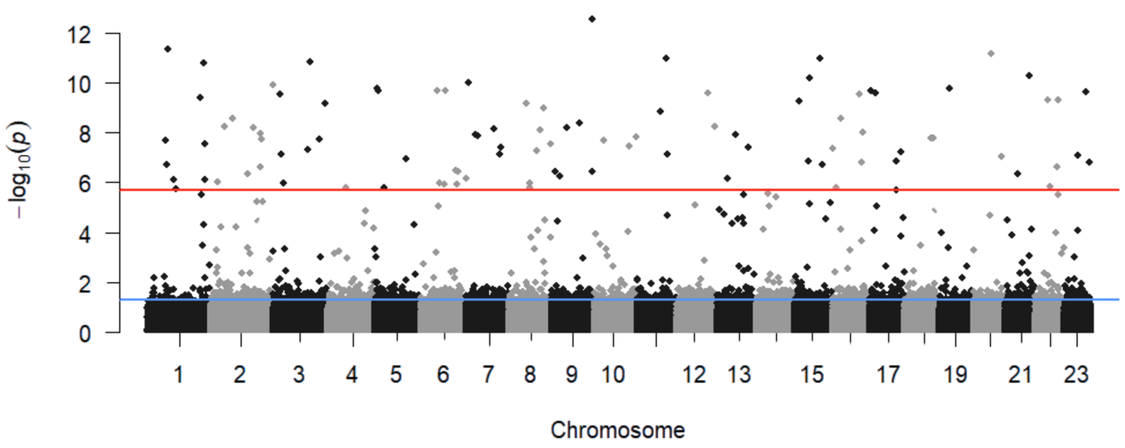


Figure 1. Manhattan plot showing the growth-associated SNPs after FDR-BY correction (p-value-0.05)

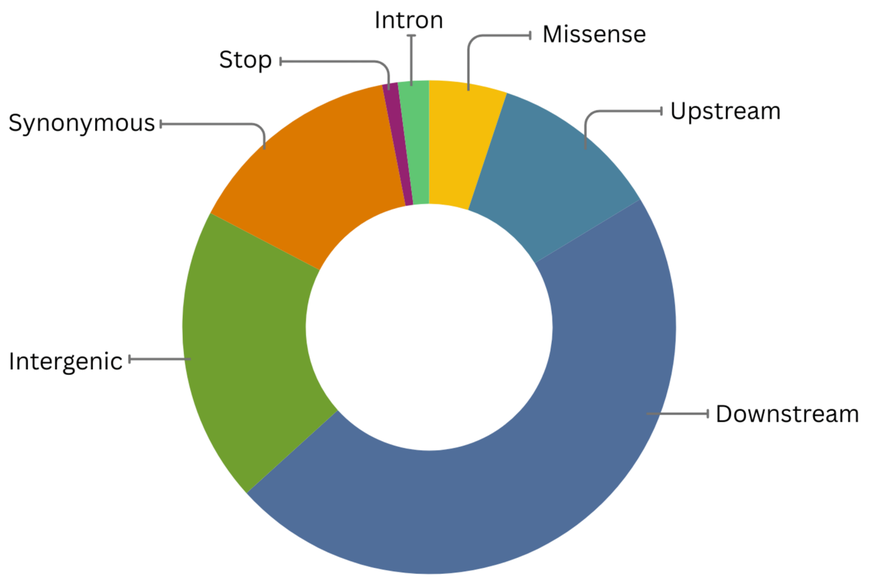


Figure 2. Distribution of growth-associated SNPs based on their effect on sequence ontology

CONCLUSION

- Growth-associated SNPs were identified as **candidate markers for selective breeding** in *Holothuria scabra*.
- Findings **support** genome-informed broodstock management, improved aquaculture productivity, sustainable production, and genetic conservation.

References:
Altamirano, J. P., & Rodriguez, J. C., Jr. (2022). Hatchery production of sea cucumbers (Sandfish *Holothuria scabra*) (Aquaculture Extension Manual No. 69). Southeast Asian Fisheries Development Center Aquaculture Department and Australian Centre for International Agricultural Research.
Juinio-Meñez, M.A. and Samonte, P.C. (2016). Harnessing S&T for a sustainable and competitive sea cucumber industry. DOST-PCAARRD S&T Media Service from: http://www.pcaarrd.dost.gov.ph/home/portal/index.php/quick-information-dispatch/2668-harnessing-s-t-for-a-sustainable-and-competitive-sea-cucumber-industry
Zhong, S., Liu, X., Ma, X., et al. (2024). Chromosomal-level genome assembly and annotation of the tropical sea cucumber *Holothuria scabra.* Scientific Data, 11, 474. https://doi.org/10.1038/s41597-024-03340-x