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Identification and assessment of differentially expressed genes involved in growth regulation in *Apostichopus japonicus*

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ABSTRACT. Rapid and efficient growth is a major consideration and challenge for global mariculture. The differential growth rate of the sea cucumber, *Apostichopus japonicus*, has significantly hampered the total production of the industry. In the present study, forward and reverse suppression subtractive hybridization libraries were constructed and sequenced from a fast-growth group and a slow-growth group of the sea cucumber. A total of 142 differentially expressed sequence tags (ESTs) with insertions longer than 150 bp were identified and further analyzed. Fifty-seven of these ESTs (approximately 40%) were functionally annotated for cell structure, energy metabolism, immunity response, and growth factor categories. Six candidate genes, arginine kinase, cytochrome *c* oxidase subunit I, HSP70, β-actin, ferritin, and the ADP-ribosylation factor, were further validated by quantitative PCR. Significant differences were found between the fast- and slow-growth groups ($P < 0.05$) for the expression levels of arginine kinase, cytochrome

c oxidase, HSP70, the ADP-ribosylation factor, and β-actin. However, no significant difference was observed for ferritin. Our results provide promising candidate gene markers for practical size screening, and also further promote marker-assisted selective breeding of this species.

Key words: *Apostichopus japonicus*; Growth rate; qPCR; Suppression subtractive hybridization

