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Molecular cloning, characterization, and expression profiles of androgen receptors in spotted scat (*Scatophagus argus*)

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ABSTRACT. Androgen plays critical roles in vertebrate reproductive systems via androgen receptors (ARs). In the present study, the full-length spotted scat (Scatophagus argus) androgen receptor (sAR) cDNA sequence was cloned from testis. The sAR cDNA measured 2448 bp in length with an open-reading frame of 2289 bp, encoding 763 amino acids. Amino acid alignment analyses showed that the sARs exhibited highly evolutionary conserved functional domains. Phylogenetically, the sARs clustered within the ARβ common vertebrate group. Real-time polymerase chain reaction (RT-PCR) revealed that sAR expression varied in level and distribution throughout the tissues of both females and males. sAR expression was detected during testicular development by quantitative RT-PCR. The results showed that the highest transcription of sARs was observed in the mid-testicular stage, and remained at a high expression level until the late-testicular stage. In addition, the effects of 17α-methyltestosterone (MT) and estrogen (E_2) on the expression of sARs in ovaries were determined using quantitative RT-PCR. sAR expression increased at 12 and 24 h post-

MT treatment and decreased with E_2 treatment. The present study provides preliminary evidence indicating gonadal plasticity of spotted scat under exogenous steroidal hormone treatments. It also provides a theoretical basis for sex reversal and production of artificial pseudo-males for female monosex breeding.

Key words: *Sarcophagus argus*; Androgen receptor; Steroid hormones; Testicular development

