# Molecular cloning and quantitative expression of sexually dimorphic markers Dmrt1 and Foxl2 during female-to-male sex change in honeycomb grouper

## PG-10 Molecular cloning and quantitative expression of sexually dimorphic markers Dmrt1 and Foxl2 during female-to-male sex change in honeycomb grouper

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The honeycomb grouper (*Epinephelus merra*) is one of the smallest members of the Serranidae family and is often used to study protogynous sex change. To determine the role of the male-determining gene Dmrt1 and the ovarian-specific dimorphic marker Foxl2 in sex change, we cloned these two markers from *E. merra* gonads by reverse transcription polymerase chain reaction (RT-PCR) and rapid amplification of cDNA ends (RACE). Two isoforms, Dmrt1a and Dmrt1b, resulted from alternative splicing in the coding region, causing the insertion of one glutamine residue in Dmrt1b. Semi-quantitative RT-PCR revealed that Dmrt1 was expressed only in the gonads, with higher levels in the testis than in the ovary. cDNA encoding Foxl2 was isolated from the ovary; Foxl2 was expressed extensively in the brain, pituitary, gonads, and gill, with its highest level in the ovary, indicating a potential role for Foxl2 in the brain–pituitary–gonad axis. Real-time quantitative RT-PCR analyses showed that Foxl2 mRNA expression was significantly downregulated from the late transitional phase to the completion of sex change. Conversely, Dmrt1 expression increased with the progression of spermatogenesis and continued until the formation of the testis. The expression profiles of these two sex-specific marker genes corresponded closely with the histological process of sex change. The down-regulation of Foxl2 most likely facilitates oocyte degeneration, whereas the up-regulation of Dmrt1 causes the proliferation of gonial germ cells into spermatogina and initiates sex change.