# The Analysis of Protein Expression Profiles in the Gonads of Tilapia(Oreochromis mossambicus)after Administration of Gon


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**ABSTRACT**

The reproductive endocrine of bony fish (teleosts) is similar to that of mammals, both are regulated by the hypothalamus-pituitary-gonadal axis. The hypothalamus secretes gonadotropin-releasing hormones (GnRHs) which stimulate the production of gonadotropin hormones (GTHs) in pituitary, and GTHs are released into the gonads by circulatory system and stimulate gonadal development, gametogenesis, emergence of secondary sex characteristics and steroidogenesis. Tilapia (Oreochromis mossambicus) is one of the most common commercial fish in Taiwan, but literature concerning the mechanism of proteins regulated in whose reproductive process is still scant. In this study, the protein expression profiles and whose correlation with reproductive system in tilapia gonads after administration of gonadotropins in vitro were analyzed by proteomic approaches. To compare the protein expression profiles of tilapia gonads, proteins from 6 groups including fresh tissue, Pre-culture (cultured in DMEM for 8 hours), 3 gonadotropin-treated groups (human chorionic gonadotropin [hCG], pregnant mare serum gonadotropin [PMSG] and hCG+PMSG) 2 hours after Pre-culture, and control (no hormone-treatment) were analyzed by using twodimensional gel electrophoresis. The results showed that combined gonadotropins treated (hCG+PMSG) group in testes had significantly higher protein spot number than that of Pre-culture group (444 ?b 8 vs. 309 ?b 44, P＜0.05), but no significant difference was observed when compared with other groups (444 ?b 8 vs. 420 ?b 14, 377 ?b 67, 389 ?b 68, and 374 ?b 62, P＞0.05). The control group of ovarian follicles had significantly lower protein spot number than others (101 ?b 4 vs. 150 ?b 15, 139 ?b 20, 139 ?b 2, and 151 ?b 35, P＜0.05), but showed no significant difference when compared with hCG group (101 ?b 4 vs. 112 ?b 14, P＞0.05). The protein spot number of deyolked ovarian follicles was significantly higher than those of undeyolked ones (101~151 vs. 260~467, P＜0.05), and the PMSG group had significantly higher protein spot number than those of other groups (467 ?b 10 vs. 297 ?b 5, 362 ?b 4, 260 ?b -vi- 4, 307 ?b 29, and 367 ?b 15, P＜0.05). The identification of significantly different protein spots by MALDI-TOF analysis showed 13 spots in testes, 6 in ovarian follicle, but only 3 in deyolked ovarian follicles. The identified proteins are related with cytoskeleton organization and structure (keratin, type II cytoskeletal 1, keratin type II cytoskeletal 2 epidermal, keratin-1, actin A3, actin cytoplasmic 1, 67 kDa cytokeratin, actin, fibrinogen beta B 1-118, fibrinopeptide B, myosin regulatory light chain 2, myosin regulatory light polypeptide 9 and Profilin-1), lipid binding and metabolism (fatty acid binding protein 7 and annexin A5), oxidoreductase activity (quinone reductase), metabolism (metallothionein and alpha-enolase), vitellogenins and some of unknown functions (onserved hypothetical protein、hypothetical protein CBG 10348 and hypothetical protein Bamb_3203). The present results suggest that the expression of tilapia gonadal proteins could be affected by gonadotropins in vitro, and these data could clarify the proteins regulating in fish reproductive process, and could be applied in reproductive endocrine research and fishery development.



Keywords : gonadotropins, tilapia, gonads, proteomics, two-dimensional gelelectrophoresis.


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