

Steroidomics: Method development and applications

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Although steroids play a broad and vital role in human physiology, they are also implicated in the development and/or progression of many cancers viz. breast, ovarian, prostate, endometrial, liver, colon, etc. as well as in neurodegenerative diseases, cardiovascular disease and obesity. Present evidence shows the involvement of steroids; such as estrogens, testosterone, bile acids, oxysterols, etc. and their metabolites in disease processes. Hence, measurement of steroids in biological samples is essential to monitor human health. Currently, there is radioimmunoassay, gas chromatography–mass spectrometry (GC/MS), and liquid chromatography–mass spectrometry (LC-MS) methods developed for steroid measurements in biological samples. However, these methods require elaborate sample preparation procedures and have concerns(s) related to reproducibility, dynamic range, time, costs, and most importantly the total coverage of steroids. Also currently, there is no method available for comprehensive steroid metabolome profiling that includes androgens, corticosteroids, progestrogens, estrogens, estrogen metabolites, bile acids, oxy sterols, neurosteroids, steroid conjugates and steroid-DNA adducts. Here, I present a global steroid metabolic profiling method based on liquid–liquid extraction (LLE) followed by ultra performance liquid chromatography (UPLC)-tandem mass spectrometry (MS/MS) for simultaneous measurement of over 100 indigenous steroids from all classes. The method was successfully applied to determine steroid hormone levels in various settings. Development of steroidomics platform and recent studies involving steroid metabolic pathways and their association with various diseases will be discussed.

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Omics in aquaculture: Applying transcriptomic and metabolomic analyses to enhance ovarian development in the black tiger shrimp *Penaeus monodon*

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Despite decades of research, the cause of delayed ovarian development in domesticated black tiger shrimp *Penaeus monodon* remained poorly understood. Thus, unilateral eyestalk ablation was routinely performed on the broodstock to force ovarian development. To circumvent this, we focused on the optimization of lipid content in shrimp feed as addition of C20:4, C20:5 and C22:6 in food pellets led to improved ovary maturation, fecundity and oogenesis in other crustaceans. Here we compared the effects of two shrimp feed: food pellets for broodstock and a live feed called polychetes *Perinereis nuntia* on shrimp ovarian maturation, gene expressions, and the lipid profiles in shrimp ovaries and hepatopancreases. Gas chromatography analysis revealed that food pellets contained more total fat, C20:5, and C22:6 than polychetes. Nevertheless, shrimp fed with polychetes still have more developed ovaries. Subsequently, HPLC analyses and enzyme immunoassays indicated that the amounts of prostaglandin E₂ (PGE₂) and prostaglandin F_{2α} (PGF_{2α}), the two C20:4-derived eicosanoids, were significantly higher in the hepatopancreas of shrimp fed with polychetes. Microarray analyses also revealed significant changes in gene expression of the eicosanoid biosynthesis pathway in both ovaries and hepatopancreases over the course of ovarian maturation. Based on these data, we believe that eicosanoids are the determining factors that regulate reproductive maturation in *P. monodon*. By understanding the dietary lipid requirements and gene regulations in female broodstock, we may be able to optimize the shrimp feed for a more sustainable shrimp larvae production in the future.

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