

The Dawn of Biotechnological Applications on Wild Harvests and Cultivated Crops

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Since the word genome (blend of word gene and chromosome) was coined in 1920 by Hans Winkler, biological research has placed great importance on the idea that genes direct all processes within a cell, and thus the organism. Underlying this concept is the assumption that proteins, via mRNA, and then metabolites are only synthesized when genes are activated. However, scientists now recognize that complex positive and negative feedback mechanisms from protein and metabolite fluxes also have major influences over gene expression. To highlight this new thinking, a radiation of biology fields under the 'omics suffix' has revolutionized biotechnological research. While a variety of new terms continue to be generated under the omics banner, the core fields of genomics (what can happen), transcript omics (what appears to happen), proteomics (what makes it happen) and metabolomics (what is happening) have produced a wealth of genotype to phenotype research avenues. This approach is facilitated by rapidly expanding bioinformatics capabilities, which allow us to mine huge amounts of data in search for often unexpected discoveries.

There are many examples of omics applications in fisheries and aquaculture. For example, transcriptomics and genetic algorithm

bioinformatics have been used to identify modes of action of toxicants to predict stress responses of fish exposed to different levels of environmental pollution. More recently, metabolomics approaches were applied to discriminate healthy from unhealthy whale sharks based on blood samples, and to monitor and manage harmful algal blooms. In aquaculture, reference libraries are being generated exponentially to be used for a variety of production purposes, such as early detection of diseases, monitoring of bacterial loads in culturing environments, optimization of hatchery rearing feeds, meat quality enhancement and even seafood authentication.

These biotechnological advances clearly provide us with powerful tools and concepts that have unimaginable potential. Indeed, this integration of nature and computers is not only re-defining the way we do science, but it is posing new challenges in data interpretation and applications. What does this information mean, how do we manage it, and how can we best utilize it? These are some of the questions that we will need to address sooner rather than later, if we want the benefits to move from the publishing arena to the production line.

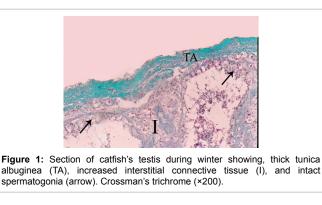
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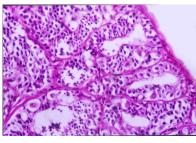


Figure 2: Section of catfish's testis during spring showing testicular lobules filled with all spermatogenic cells. H&E (×200).

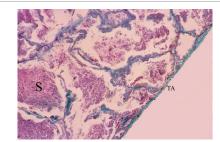


Figure 3: Section of catfish's testis during summer showing, thin tunica albuginea (TA) compared to Figure 1. Testicular lobules are filled with spermatozoa (S). Crossman's trichrome (×100).

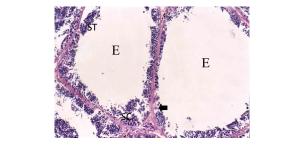


Figure 4: Section of catfish's testis during autumn showing, empty testicular lobules (E). Notice all developmental stages; spermatogonia (arrow), spermatocytes cyst (SC), spermatid cyst (ST). PAS technique (×200).

	Winter	Spring	Summer	Autumn
Male catfish	1.07	3.6	4.0	2.2
Female catfish	9.3	26.4	30.7	18.8

Table 1: GSI values for male and female catfishes during different seasons of the year.

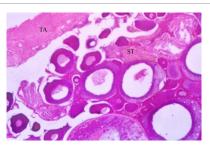


Figure 5: Section of catfish's ovary during winter showing, very thick tunica albuginea (TA) and increased stromal connective tissue (ST). Notice the degenerated follicles. PAS technique (X400).

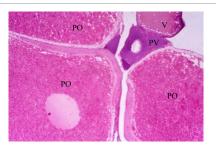


Figure 6: Section of catfish's ovary during spring showing, pre-vitellogenic follicles (PV), vitellogenic follicles (V) and many post-vitellogenic follicles (PO). H&E (X400).

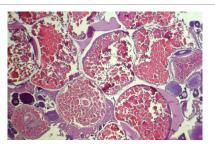


Figure 7: Section of catfish's ovary during summer showing, abundant mature follicles (MF). H&E (X40).

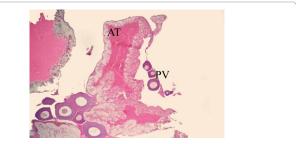


Figure 8: Section of catfish's ovary during autumn showing, predominance of atretic (AT) and pre-vitellogenic follicles (PV). H&E (X200).