

次世代シーケンサーによるライギョダマシ脾臓 RNA のトランスクリプトーム解析

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Transcriptomic analysis of Antarctic toothfish spleen RNA by next generation sequencer

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Notothenioid fish, the dominant species in the Southern Ocean, is one of the most intriguing group of species from evolutionary viewpoint. One major reason of their evolutionary success is the acquisition of anti-freeze glycopeptides (AFGP) by the modification of trypsinogen, which enables them to survive even under harsh environment of the Southern Ocean where temperature can become as low as about -2°C . Another peculiar example of adaptive evolution is nonfunctionalization of hemoglobin genes in icefish. Although loss of hemoglobin is generally lethal for vertebrates, extensive modification of cardiovascular system in icefish has compensated such disadvantage with ensuring sufficient oxygen transport. Recent studies of mitochondrial genes, furthermore, have shown that the evolutionary rates of genes involved in cellular respiration are much higher compared with other teleosts (see also Nagata and Ota in this symposium).

In order to shed light on the molecular evolution of notothenioid genes in larger scale, we are currently investigating the genes expressed in Antarctic toothfish (*Dissostichus mawsoni*) spleen, one of important tissue of hematopoiesis, with taking advantage of technological progress of next generation sequencer. So far 55180 nucleotide sequences were assembled from about 11 million 50-mers by using velvet program (table 1). Subsequent analysis of assembled sequences then revealed that genes highly expressed are those involved in protein synthesis and folding, protein degradation, cellular respiration, cellular movement, innate and adaptive immunity, oxygen transport, iron ion storage and homeostasis, and protection against freezing, as shown in table 2. In the presentation, I am going to further discuss the results obtained in detail from molecular evolutionary perspectives.

Table 1. Number of assembled nucleotide sequences*

Size of sequences (bp)	Number of sequences
100 ~ 199	33253
200 ~ 299	5714
300 ~ 399	1774
400 ~ 499	812
500 ~ 599	382
600 ~ 699	201
700 ~ 799	139
800 ~ 899	67
900 ~ 999	48
1000 ~ 1099	33
1100 ~ 1199	20
1200 ~ 1299	19
1300 ~ 1399	8
1400 ~ 1499	2
1500 ~ 1599	4
1600 ~ 1699	6
1700 ~ 1799	4
1800 ~	4

*The largest nucleotide sequence assembled is the elongation factor 2 (2473bp).

Table 2. Highly expressed genes**

Gene
1. rRNA promoter binding protein
2. astacin like metalloprotease
3. β actins
4. complement molecules
5. elongation factors
6. thymosin β
7. immunoglobulins
8. type II antifreeze proteins
9. peptidyl-prolyl cis-trans isomerase
10. β_2 -microglobulin
11. hemoglobins
12. trypsinogens (or chimeric AFGP/ trypsinogen -like protease)
13. ferritins
14. heat shock protein 70
15. hepcidin
16. C-C motif chemokine
17. profilin
18. carboxypeptidase

** Excluding ribosomal genes, mitochondrial genes and genes whose function were unknown.