Lipid metabolism in conger eel (*Conger myriaster*) during artificially induced ovarian development

Guixiang Wang, Kang Li, Rucong Liu, Zhixin Jiang, Tiezhu Li, Xubing Ba, Liping Liu*

a Key Laboratory of Exploration and Utilization of Aquatic Genetic Resources, Ministry of Education, Shanghai Ocean University, Shanghai 201306, China;

b Shanghai Engineering Research Center of Aquaculture, Shanghai Ocean University, Shanghai 201306, China;

c National Demonstration Center for Experimental Fisheries Science Education, Shanghai Ocean University, Shanghai 201306, China

Introduction

Conger eel (Conger myriaster) farming is completely dependent on wild eel seedlings, which severely restricts the healthy development of the industry.

During the development of the eel, the conversion of lipids is closely related to the development of the eel's gonadal and the quality of the eggs.

Lipidomic analysis is a systematic study of whole lipids, revealing the role of lipids in life activities.

Materials and Methods

After extracting total lipids from liver, gonads, muscle and plasma, the samples of the four tissues and QC samples were tested on the computer using UPLC-MS (Fig.1), and the raw data was imported into the lipidomics processing software Progenesis QI (Waters Corporation, Milford, USA) After analysis, PCA and OPLS-DA were performed in SIMCA-14.1 software (Umetrics), VIP>1, p<0.05 The lipids are significantly different lipids. Use online databases such as HMDB, LIPIDMAPS and MetaboAnalyst 5.0 to confirm the structure of differential lipids and lipid markers.



Fig.1 UPLC-MS sampling system

Results

1. Analysis of lipid metabolism in main tissues of conger eel at different developmental stages







Notes:(1) liver (ESI+), (2) liver (ESI-), (3) muscle (ESI+), (4) muscle (ESI-), (5) gonad (ESI+), (6) gonad (ESI-), (7) plasma (ESI+), (8) plasma (ESI-)

2.Identification of lipid markers

Table.1 Summary of four types of tissue lipid markers														
Compound name	PS	PE	PI	PC	PA	PG	TG	SM	DG	Cer	CL	CE	FFA	Total
Liver(kinds)	3	15	2	15	1	1	20	1	1	3	5		1	68
Muscle(kinds)		10	3	4			9						1	27
Gonad(kinds)	2	26	4	15		1	5	4		3			3	63
Plasma(kinds)	3	72	8	87			23	13		2	-	1	1	212

Notes: PS-phosphatidylserine, PE-phosphatidylethanolamine, PI-phosphatidylinositol, PC-phosphatidylcholine, PA-phosphatidic acid, PG-Phosphatidylglycerol, TG- triglycerides, SM-sphingomyelin, DG-diglyceride, Cer-ceramide, CL-cardiolipin, CE-cholesteryl ester, FFA-Free Fat Acid

3.Heat map analysis of relative content of lipid markers







The relative content of lipid markers in liver, muscle, gonads and different at plasma gonadal of stages development in conger eel is shown in the figure(Fig.3). Different lipids have different mobilization conditions at different stages of development.

Fig.3 Heat map analysis of relative content of four tissue lipid markers Notes: (1) liver, (2) muscle, (3) gonad, (4) plasma

4. Changes in the activity of lipid metabolism-related enzymes in the liver



Fig.4 Lipid metabolism-related enzyme activities at different stages

Notes: 1. chromatin nucleolus stage, 2. oil droplet stage, 3. primary yolk globule stage, 4. secondary yolk globule stage 5. migratory nucleus stage 6. maturation stage,(1) Fatty acid synthase enzyme ,(2) Liver lipase enzyme ,(3) Lipoprotein lipase enzyme

Summary

Studies have shown that during the artificial induction of ovarian development in conger eel, TG, PC, PE and SM are mobilized for gonadal development, fatty acid synthase, liver lipase and lipoprotein lipase promotes the mobilization of main lipids. This experiment explored the changes in lipid metabolism during the artificial reproduction of the conger eel, in order to provide a basis for the sustainable development of the conger eel fishery, thereby increasing the number of wild populations.

Contact

Guixiang Wang,

Key Laboratory of Exploration and Utilization of Aquatic Genetic Resources, Ministry of Education, Shanghai Ocean University, Shanghai, China Email: m190100332@st.shou.edu.cn