

Editorial

# Food Chains and Food Webs in Aquatic Ecosystems

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**Abstract:** Food chains and food webs describe the structure of communities and their energy flows, and they present interactions between species. Recently, diverse methods have been developed for both experimental studies and theoretical/computational studies on food webs as well as species interactions. They are effectively used for various applications, including the monitoring and assessment of ecosystems. This Special Issue includes six empirical studies on food chains and food webs as well as effects of environmental factors on organisms in aquatic ecosystems. They confirmed the usefulness of their methods including isotope, DNA-barcoding with gut contents, and environmental DNA for biological monitoring and ecosystem assessment.

**Keywords:** food web; food chain; aquatic ecosystems; monitoring; assessment; environmental DNA; isotope; NGS

## 1. Introduction

It is important to understand the role and function between organisms' interactions in the food web of the aquatic ecosystem. The key biological interaction in the aquatic food web is matter cycling mediated by the food chain, and predation often works as a regulating factor for energy pathways, as well as determining species composition in the ecosystem [1]. In particular, the food sources at the species levels are critical components linking organisms with larger predatory species such as crustaceans and fish within the grazing food chain: rotifers-copepods, micro/macroinvertebrates, and larval/mature fish [2,3]. Consequently, they function as a channel for the flux of organic matter within diverse organism assemblages organized in an intermediate position between the two different food webs, and a way of transferring nutrients and energy from the prey species–predator species loop to higher trophic levels. Thus, the biological prey–predation interactions in the food web are receiving great attention to understand not only the interrelated biological relationships but also the structure and function of aquatic food webs [4].

In recent years, genomic and next-generation sequencing (NGS) technologies have developed rapidly and been applied to the ecological domain. Meta-barcoding techniques have accreted the reliability of identifying specific taxonomic groups of organisms at both species and genus level [5], and environmental DNA (eDNA) have enabled the detection of invisible species in various situations [6,7]. The eDNA approaches have also been used to clarify and understand systematic ecology, particularly biological trophic interaction in both aquatic habitat environments and food webs by collecting information from food sources found in gut contents of species and the excrement of lived organisms. This helps to overcome unidentified limitations of food source analyses, which were based on microscopic analysis [8–11]. At present, it is necessary to develop a method to separate pure gut content from target organisms for a wide range of applications of DNA technology in food source identification. In addition, the most fundamental methodology is to produce a framed “blocking primer”, which removes the DNA of the target species from the target gut contents.

On the other hand, changes in temperature, salinity, and metal contamination could affect the uptake, elimination, and biotransformation rates of common organisms [12]. Increasing water temperatures can act as a stressor that impacts the immune and physical responses of aquatic organisms, especially the cascading food chain network linking of plankton–invertebrates–fish communities. Accordingly, a temperature change can significantly affect food chains' related development and the health of aquatic prey and predation organisms. Further, temperature is known to have a significant effect on oxidative stress biomarkers for aquatic organisms. Due to the fact that climate change is expected to result in more frequent and intense heat shock events, it is pertinent to investigate the effect of increasing temperatures on the oxidative stress response of common aquatic organisms.

Oxidative stress is induced by a wide range of environmental components including temperature changes, UV stress, chemical action and oxygen shortages, and an over-production of reactive oxygen species (ROS) in relation to defense mechanisms [13]. The overproduction of ROS can generate oxidative stress which leads to permanent cell damage. Thus, the intracellular accumulation of ROS would not only disrupt the functions of specific tissues and organs but also lead to the premature death of the entire organism [14]. Oxidative stress biomarkers have been widely used in the development of ecological indices and in the assessment of the exposure of aquatic organisms to contaminants from agricultural, industrial, and urban pollution [15]. Oxidative stress is also involved in many biological and pathological processes and normal physiological development [13]. Currently, the study of many molecular markers has been developed in order to understand the physiological response of organisms. Superoxide dismutases (SODs) and catalase (CAT) are important antioxidant enzymes to protect the cell from oxidative damage by ROS. Especially, heat shock protein 90 (HSP90), a highly conserved protein, is a dimer that binds to several cellular proteins, including steroid receptors and protein kinases [16,17]. In aquatic animals, the induction of HSP90 genes and HSPs family has been widely reported in response to cellular stress, including temperature elevation, osmotic stress, hormone stimulation, herbicide toxicity, and viral infections [18,19].

This Special Issue (“Food Chains and Food Webs in Aquatic Ecosystems”) aims to share recent information on the study for food chains and food webs in aquatic ecosystems focusing on biological monitoring and assessment of aquatic ecosystems.

## 2. Papers in This Special Issue

The six papers included in this Issue focus on food chains and food webs in aquatic ecosystems as well as on effects of environmental factors.

To test a hypothesis that differences in invertebrate and fish assemblages in lakes characterized by different trophic conditions determine patterns of variation in the trophic niche width of the fish species depending on their specific feeding habits, Caputi et al. [20] studied the feeding behavior of two omnivorous species (*Anguilla anguilla* and the seabream *Diplodus annularis*), which are ecologically and economically important, using the stable isotope analysis of carbon ( $\delta^{13}\text{C}$ ) and nitrogen ( $\delta^{15}\text{N}$ ). They found that *A. anguilla* was a generalist in the eutrophic lake, whereas *D. annularis* became more specialist, suggesting that changes in macroinvertebrate and fish community composition affect the trophic strategies of high-trophic level consumers.

Identification of gut contents is helpful to analyze the food source of animals. However, it has several limitations such as small size and fragmentation of gut materials. To overcome these limitations, recently, genomic approaches have been applied to understand the biological interaction including food webs [9,10,21]. Oh et al. [21] proposed a pretreatment method for DNA-barcoding to analyze gut contents of rotifers to provide a better understanding of rotifer food sources and showed that the proposed method is useful to identify food sources of small organisms.

Jo et al. [22] and Kim et al. [23] presented the application of eDNA in costal aquatic ecosystems. Jo et al. [22] determined aquatic community taxonomic composition using eDNA based on an NGS and analyzed the community spatial distribution with regard to environmental parameters and the habitat types. Meanwhile, Kim et al. [23] compared water sampling between the eDNA method and

conventional microscopic identification for plankton community composition related to ecological monitoring and assessment of aquatic ecosystems. They found that the eDNA approach provides a wider variety of species composition, while conventional microscopic identification depicts more distinct plankton communities in sites, suggesting that the eDNA approach is a valuable alternative for biological monitoring and diversity assessments in aquatic ecosystems.

Kim et al. [24] assessed the spatial distribution of benthic macroinvertebrate communities responding to their environment such as land use and water quality, and concluded that information such as land use which is easily available characterized effectively the distribution of benthic macroinvertebrates.

To evaluate the toxic effects of di-2-ethylhexyl phthalate (DEHP) on cellular protection in *Macrophthalmus japonicus* crabs, Park et al. [25] identified two stress-related genes and investigated the genomic structure, phylogenetic relationships with other homologous heat shock proteins (HSPs), and transcriptional responses of HSPs under DEHP stress. Their results suggested that DEHP toxicity could disrupt cellular immune protection through transcriptional changes to HSPs in the test organisms.

### 3. Conclusions

Food chains and food webs describe the structure of communities and their energy flows, and they present interactions between species. Recently, diverse methods have been developed for both experimental studies and theoretical/computational studies. They improve our fundamental ecological knowledge and are effectively used for various applications, including the monitoring and assessment of ecosystems. In particular, ecological monitoring and assessment have advanced in recent decades. Along with the progress of molecular and eDNA techniques, the process of monitoring and assessment has become rapid and accurate. A wide variety of ecological disturbances associated with temperature and salinity changes and other environmental factors are being recognized as threats to the food chain functions of freshwater and marine ecosystems.

This Special Issue included empirical studies on food chains and food webs in aquatic ecosystems. They confirmed the usefulness of their methods including isotope, DNA-barcoding with gut contents, and eDNA for biological monitoring and ecosystem assessment. In further studies, however, theoretical and computational approaches including food web modelling and network analyses are expected to characterize quantitatively the interactions among species as well as ecosystem structures and dynamics through the collaborative works between experimental and computational scientists.

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### References

1. Carrillo, P.; Medina-Sánchez, J.; Villar-Argaiz, M.; Delgado-Molina, J.; Bullejos Carrillo, F.J. Complex interactions in microbial food webs: Stoichiometric and functional approaches. *Limnetica* **2006**, *25*, 189–204.
2. Wallace, R.L.; Snell, T.W.; Claudia, R.; Thomas, N. *Rotifera Vol. 1: Biology, Ecology and Systematics*, 2nd ed.; Backhuys: Leiden, The Netherlands, 2006.

3. Pree, B.; Larsen, A.; Egge, J.K.; Simonelli, P.; Madhusoodhanan, R.; Tsagaraki, T.M.; Våge, S.; Erga, S.R.; Bratbak, G.; Thingstad, T.F. Dampened copepod-mediated trophic cascades in a microzooplankton-dominated microbial food web: A mesocosm study. *Limnol. Oceanogr.* **2017**, *62*, 1031–1044. [[CrossRef](#)]
4. Oh, H.-J.; Jeong, H.-G.; Nam, G.-S.; Oda, Y.; Dai, W.; Lee, E.-H.; Kong, D.; Hwang, S.-J.; Chang, K.-H. Comparison of taxon-based and trophi-based response patterns of rotifer community to water quality: Applicability of the rotifer functional group as an indicator of water quality. *Anim. Cells Syst.* **2017**, *21*, 133–140. [[CrossRef](#)]
5. Hebert, P.D.N.; Cywinska, A.; Ball, S.L.; Dewaard, J.R. Biological identifications through DNA barcodes. *Proc. R. Soc. Lond. Ser. B Biol. Sci.* **2003**, *270*, 313–321. [[CrossRef](#)]
6. Barnes, M.A.; Turner, C.R. The ecology of environmental DNA and implications for conservation genetics. *Conserv. Genet.* **2016**, *17*, 1–17. [[CrossRef](#)]
7. Kress, W.J.; García-Robledo, C.; Uriarte, M.; Erickson, D.L. DNA barcodes for ecology, evolution, and conservation. *Trends Ecol. Evol.* **2015**, *30*, 25–35. [[CrossRef](#)] [[PubMed](#)]
8. Symondson, W.O.C. Molecular identification of prey in predator diets. *Mol. Ecol.* **2002**, *11*, 627–641. [[CrossRef](#)] [[PubMed](#)]
9. Carreon-Martinez, L.; Johnson, T.B.; Ludsins, S.A.; Heath, D.D. Utilization of stomach content DNA to determine diet diversity in piscivorous fishes. *J. Fish Biol.* **2011**, *78*, 1170–1182. [[CrossRef](#)] [[PubMed](#)]
10. Jo, H.; Gim, J.-A.; Jeong, K.-S.; Kim, H.-S.; Joo, G.-J. Application of DNA barcoding for identification of freshwater carnivorous fish diets: Is number of prey items dependent on size class for *Micropterus salmoides*? *Ecol. Evol.* **2014**, *4*, 219–229. [[CrossRef](#)]
11. Jo, H.; Ventura, M.; Vidal, N.; Gim, J.-S.; Buchaca, T.; Barmuta, L.A.; Jeppesen, E.; Joo, G.-J. Discovering hidden biodiversity: The use of complementary monitoring of fish diet based on DNA barcoding in freshwater ecosystems. *Ecol. Evol.* **2016**, *6*, 219–232. [[CrossRef](#)]
12. Lydy, M.J.; Belden, J.B.; Ternes, M.A. Effects of temperature on the toxicity of m-parathion, chlorpyrifos, and pentachlorobenzene to *Chironomus tentans*. *Arch. Environ. Contam. Toxicol.* **1999**, *37*, 542–547. [[CrossRef](#)]
13. Wu, C.; Zhang, W.; Mai, K.; Xu, W.; Zhong, X. Effects of dietary zinc on gene expression of antioxidant enzymes and heat shock proteins in hepatopancreas of abalone *Haliotis discus hannai*. *Comp. Biochem. Physiol. Part C Toxicol. Pharmacol.* **2011**, *154*, 1–6. [[CrossRef](#)]
14. Carnevali, S.; Petruzzelli, S.; Longoni, B.; Vanacore, R.; Barale, R.; Cipollini, M.; Scatena, F.; Paggiaro, P.; Celi, A.; Giuntini, C. Cigarette smoke extract induces oxidative stress and apoptosis in human lung fibroblasts. *Am. J. Physiol. Lung Cell. Mol. Physiol.* **2003**, *284*, L955–L963. [[CrossRef](#)]
15. Vinagre, C.; Madeira, D.; Mendonça, V.; Dias, M.; Roma, J.; Diniz, M.S. Effect of increasing temperature in the differential activity of oxidative stress biomarkers in various tissues of the Rock goby, *Gobius paganellus*. *Mar. Environ. Res.* **2014**, *97*, 10–14. [[CrossRef](#)] [[PubMed](#)]
16. Pratt, W.B. The role of heat shock proteins in regulating the function, folding, and trafficking of the glucocorticoid receptor. *J. Biol. Chem.* **1993**, *268*, 21455–21458. [[PubMed](#)]
17. Csermely, P.; Schnaider, T.; Soti, C.; Prohászka, Z.; Nardai, G. The 90-kDa molecular chaperone family: Structure, function, and clinical applications. A comprehensive review. *Pharmacol. Ther.* **1998**, *79*, 129–168. [[CrossRef](#)]
18. Chang, E.S.; Chang, S.A.; Kwillwe, R.; Reddy, P.S.; Snyder, M.J.; Spees, J.L. Quantification of stress in lobsters: Crustacean hyperglycemic hormone, stress proteins, and gene expression. *Am. Zool.* **1999**, *39*, 487–495. [[CrossRef](#)]
19. Park, K.; Park, J.; Kim, J.; Kwak, I.-S. Biological and molecular responses of *Chironomus riparius* (Diptera, Chironomidae) to herbicide 2,4-D (2,4-dichlorophenoxyacetic acid). *Comp. Biochem. Physiol. Part C Toxicol. Pharmacol.* **2010**, *151*, 439–446. [[CrossRef](#)]
20. Caputi, S.S.; Careddu, G.; Calizza, E.; Fiorentino, F.; Maccapan, D.; Rossi, L.; Costantini, M.L. Changing isotopic food webs of two economically important fish in Mediterranean coastal lakes with different trophic status. *Appl. Sci.* **2020**, *10*, 2756. [[CrossRef](#)]
21. Oh, H.-J.; Krogh, P.; Jeong, H.-G.; Joo, G.-J.; Kwak, I.-S.; Hwang, S.-J.; Gim, J.-S.; Chang, K.-H.; Jo, H. Pretreatment method for DNA barcoding to analyze gut contents of rotifers. *Appl. Sci.* **2020**, *10*, 1064. [[CrossRef](#)]
22. Jo, H.; Kim, D.-K.; Park, K.; Kwak, I.-S. Discrimination of spatial distribution of aquatic organisms in a coastal ecosystem using eDNA. *Appl. Sci.* **2019**, *9*, 3450. [[CrossRef](#)]

23. Kim, D.-K.; Park, K.; Jo, H.; Kwak, I.-S. Comparison of water sampling between environmental DNA metabarcoding and conventional microscopic identification: A case study in Gwangyang Bay, South Korea. *Appl. Sci.* **2019**, *9*, 3272. [[CrossRef](#)]
24. Kim, D.-K.; Jo, H.; Park, K.; Kwak, I.-S. Assessing spatial distribution of benthic macroinvertebrate communities associated with surrounding land cover and water quality. *Appl. Sci.* **2019**, *9*, 5162. [[CrossRef](#)]
25. Park, K.; Kim, W.-S.; Kwak, I.-S. Effects of di-(2-ethylhexyl) phthalate on transcriptional expression of cellular protection-related HSP60 and HSP67B2 genes in the mud crab *Macrophthalmus japonicus*. *Appl. Sci.* **2020**, *10*, 2766. [[CrossRef](#)]



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