ABSTRACT BOOK

4TH INTERNATIONAL SYMPOSIUM OF BENTHOLOGICAL SOCIETY OF ASIA

Nanjing, the People's Republic of China

21-25 August, 2018

Human population and economic growth continue to degrade freshwater ecosystem health greatly and to threaten aquatic biodiversity throughout Asia. To contribute to useful solutions for improving the health and biodiversity of Asia's freshwater ecosystems, the Benthological Society of Asia (BSA) has chosen "Freshwater Health and Biodiversity in Asia" as the theme for its 2018 biennial symposium. The 4th International Symposium of the Benthological Society of Asia (BSA2018) will be held in Nanjing, 21–25 August 2018. The 2nd Youth Freshwater Ecology School will be held 19–20 August 2018 just prior to the BSA2018.

As hosts of the Symposium, Nanjing Agricultural University, Nanjing Normal University, and Xi'an Jiaotong-Liverpool University warmly welcome you to join this Symposium to discuss the theme and its related topics; meet other scientists, educators, practitioners and policy-makers; and make new friends from Asia and the rest of the world.

SESSIONS	
S01	Asian freshwater biomonitoring and bioassessment: methods, perspectives and challenges
S02	Benthos biodiversity conservation and rehabilitation
S03	Impacts on community structure and function
S04	Taxonomy, evolution, and systematics
S05	Population, assemblage, and community ecology

BSA
The Benthological Society of Asia

THE BENTHOLOGICAL SOCIETY OF ASIA

NANJING AGRICULTURAL UNIVERSITY

NANJING NORMAL UNIVERSITY

XI'AN JIAOTONG-LIVERPOOL UNIVERSITY

INDEX

ORAL SESSION

Title	Authors	Page
S01: Asian Freshwater Biomonitoring and Bioassessment: Methods, Perspectives and Challenges		
INCORPORATING TRAIT AND FUNCTIONAL DIVERSITY TO ENHANCE MULTIMETRIC INDEX PERFORMANCE AND ASSESS LAND USE GRADIENTS	CHEN K., HUGHES R.M., OLSON J.R., WANG B.X.	1
METABARCODING BASED MACROINVERTEBRATE COMMUNITY ASSESSMENT UNDER THE INFLUENCE OF ARTIFICIAL GRAVEL BARS IN THE DOWNSTREAM OF DAM IN TRINITY RIVER	LI B., S J., S T., T Y., W K.	2
DEVELOPMENT AND APPLICATION OF A MACROINVERTEBRATE-BASED INDEX OF BIOTIC INTEGRITY IN NORTHERN RIVER OF CHINA: A CASE STUDY OF SONGHUA RIVER	LIN K.X., LI L., LIU L.S., LIU Y.L.	3
THE APPLICABILITY ASSESSMENT OF CANDIDATE AQUATIC SPECIES USED TO ONLINE BEHAVIOURAL MONITORING BASED ON QUANTITATIVE ION CHARACTER-ACTIVITY RELATIONSHIPS (QICARS) AND EXPERIMENTAL EXPOSURES TO HEAVY METHALS	LIU Y.D., WANG H., LIU Z.Y., CHEN X.L., WU F.C., GIESY J.P.	4
USE OF AQUATIC INSECTS AS BIOINDICATORS OF WATER QUALITY IN KWAN PHAYAO, PHAYAO PROVINCE, NORTHERN THAILAND	PHOSANGA K., JAITRONG B., JITMANEE C.	5
FLUCTUATING ASYMMETRY IN POLLUTION-TOLERANT CADDISFLY *HYDROPSYCHE DOCTERSI* AS AN INDICATOR OF RIVER CONDITION	SUHAILA A.H., MOHD FAKHRULLAH SALAFUSALAM M.A.	6
THE USE OF BENTHIC MACROINVERTEBRATES AS BIOINDICATORS FOR EVALUATING OF WATER QUALITY OF RIVERS IN RAINY SEASON, THAILAND	TECHAKIJVEJ C., PHALARAKSH C.	7
THE ASSESSMENT OF LARGE RIVER HEALTH USING BENTHIC-INDEX OF BIOTIC INTEGRITY — A CASE STUDY IN DONGJIANG RIVER OF THE PEARL BASIN	WU J.Y., PENG Z.H., WANG H.Z., CUI Y.D.	8
S02: Benthos Biodiversity Conservation and Rehabilitation		
STUDY ON CONSERVATION OF FRESHWATER MOLLUSCA DIVERSITY IN THE YANGTZE RIVER BASIN ON MAXENT MODEL	HE Y.J., WANG H.Z., CUI Y.D., SHU F.Y., WANG H.J.	9
BIODIVERSITY OF AQAUTIC INSECTS IN KWAN PHAYAO, PHAYAO PROVINCE, NORTHERN THAILAND	JAITRONG B., PHOSANGA K., JITMANEE C.	10
INITIAL ESTABLISHMENT OF ROUTING MONITORING AND ASSESSMENT METHODS FOR ECOLOGICAL DREDGING EFFECTS ON MACROINVERTEBRATE COMMUNITY IN TAIHU LAKE	LU H.M., WU J.B., WANG B.X., CHEN L.M., LI X.H.	11
GENETIC CHARACTERISTICS OF THE ASIAN GIANT WATER BUGS, *LETHOCERUS DEYROLLEI* AND *L. INDICUS* (HEMIPTERA: BELOSTOMATIDAE) IN ASSOCIATION WITH ARTIFICIAL LIGHT	SAREEIN N., KANG J.H., YOON T.J., PHALARAKSH C., BAE Y.J.	12
MACROZOOBENTHOS COMMUNITY STRUCTURE AND ENVIRONMENTAL DETERMINANTS OF LIUXI RIVER IN GUANGZHOU	YAO K.S., CUI Y.D.	13

Title	Authors	Page
S03: Impacts on Community Structure and Function		
TRAITS UNDERDISPERSION AND OVERDISPERSIOIN OF BENTHIC MACROINVERTEBRATE IN THREE CHINESE WATERSHEDS ACROSS TROPICAL TO SUB-TROPICAL REGIONS AND THE EFFECT OF ENVIRONMENTAL CONSTRAINTS	DING N., WANG B.X., CORNELISSEN J.H.C., BERG M.P., CHEN K.	14
SENSITIVE TRAITS AND TRAITS COMBINATIONS REVEAL THE FUNCTIONAL DIVERSITY DECLINE OF STREAM MACROINVERTEBRATE ASSEMBLAGES IN RESPONSE TO URBANIZATION	GAO J., WANG B.X., CHEN K., RAJPER A.R.	15
SECONDARY SUCCESSION OF BENTHIC MACROINVERTEBRATE COMMUNITIES IN THE HAN RIVER IN SEOUL, KOREA	PARK S.H., SEOK S.W., BAE Y.J.	16
EFFECT OF WATERSHED URBANIZATION ON EPT (EPHEMEROPTERA, PLECOPTERA AND TRICHOPTERA) COMMUNITY IN THE MIDDLE QIANGTANG RIVER BASIN, ZHEJIANG PROVINCE, CHINA	RAJPER A.R., HE S.W., CHEN K., MBAO E., ZHANG J.W., WANG B.X.	17
SEASONAL VARIATION OF THE IMPACTS OF AGRICULTURE ON MACROINVERTEBRATE FUNCTIONAL TRAITS AND FUNCTIONAL DIVERSITY IN HIGH LATITUDE STREAMS	WANG L., YANG H.J., GAO Y.Z.	18
EFFECTS OF ANTHROPOGENIC SUBSIDY AND GLYPHOSATE ON MACROINVERTEBRATE ASSEMBLAGES IN STREAMS	XIANG H.Y., ZHANG Y.X., ATKINSON D., RAJU S.	19
NUTRIENT ENRICHMENT HOMOGENIZES TAXONOMIC AND FUNCTIONAL DIVERSITY OF BENTHIC MACROINVERTEBRATE ASSEMBLAGES IN SHALLOW LAKES	ZHANG Y., CHENG L., LI K.Y., ZHANG L., CAI Y.J., WANG X.L., HEINO J.	20
S04: Taxonomy, Evolution, and Systematics		
STUDY ON TAXONOMY OF CHIRONOMINAE IN ZHEJIANG PROVINCE (DIPTERA, CHIRONOMIDAE)	KONG Q.Q., LI Y.L., LIN X.L., WANG X.H., QI X.	21
ASSEMBLING A COMPREHENSIVE DNA BARCODE REFERENCE LIBRARY FOR CHINESE NON-BITING MIDGES (DIPTERA: CHIRONOMIDAE)	LIN X.L., WANG X.H.	22
THE LARVAE OF *EPEORUS DAYONGENESIS* AND *E. HERKLOTSI* FROM CHINA (EPHEMEROPTERA: HEPTAGENIIDAE)	MA Z.X., ZHANG W., HAN N., ZHOU C.F.	23
OVERVIEW OF PHILIPPINE STONEFLIES (INSECTA: PLECOPTERA) WITH NEW RECORDS OF *NEOPERLA* NEEDHAM, 1905 FROM MINDORO ISLAND	PELINGEN A.L., FREITAG H.	24
TAXONOMY AND DISTRIBUTION OF AQUATIC OLIGOCHAETES (ANNELIDA: OLIGOCHAETA) IN TIBET, CHINA	PENG Y., CUI Y.D.	25
ANALYSIS OF TAXONOMY OF FAR EASTERN UNIONINAE AND ANODONTINAE (UNIONIDAE, BIVALVIA)	SAYENKO E.M., SOROKA M.	26
AN EVOLUTIONARY ECOLOGICAL STUDY OF THE GIANT WATER BUG *APPASUS JAPONICUS*: DETECTION OF THEM EXHIBITING ASYMMETRIC REPRODUCTIVE ISOLATION	SUZUKI T., TOJO K.	27
EXTREMELY LARGE GENETIC DIFFERENTIATION IN THE MAYFLY *DIPTEROMIMUS TIPULIFORMIS*: AN IDEAL CASE IN ELUCIDATION OF THE MECHANISMS OF SPECIATION (EPHEMEROPTERA; DIPTEROMIMIDAE)	TAKENAKA M., TOJO K.	28
TAXONOMY OF THE FAMILY BAETIDAE (INSECTA: EPHEMEROPTERA) IN CHINA	TONG X.L., SHI W.F.	29
PHYLOGENY OF THE SUBFAMILY MACRONEMATINAE (TRICHOPTERA: HYDROPSYCHIDAE) BASED ON MOLECULAR AND MORPHOLOGICAL ANALYSES	UY CHRISTINE J. C., KANG J.H., BAE Y.J.	30
GENETIC DIVERSITY OF *CLOEON* SPECIES IN EAST ASIA: WITH SPECIFICAL REFERENCE TO THE SPECIFIC LINEAGE OF *CLOEON DIPTERUM*	YANO K., TOJO K.	31

Title	Authors	Page
A REVISED REVIEW ON *CINYGMINA* OF CHINA (EPHEMEROPTERA: HEPTAGENIIDAE: ECDYONURINAE)	ZHANG W., MA Z.X., HAN N., ZHOU C.F.	32
MOLECULAR IDENTIFICATION OF THE INTERMEDIATE OF TWO PROXIMAL SPECIES OF *LIMNODRILUS* (OLIGOCHAETA, NAIDIDAE) BASED ON 16S RDNA AND COI SEQUENCES	ZHOU T.T., PENG Y., CUI Y.D.	33
S05: Population, Assemblage, and Community Ecology		
LAND USE CHANGES AND SOCIO-ECONOMIC DEVELOPMENT DETERIORATING RIVER ECOSYSTEM HEALTH IN HAIHE RIVER BASINS, CHINA	CHENG X., SUN R.H., WU D.Y.	34
COMMUNITY AND POPULATION DYNAMICS OF BENTHIC MACROINVERTEBRATES IN RESPONDING TO DISTURBANCES IN STREAMS	CHON T.S., KWAK G., JANG Y.H., JUNG N., LEEM J.B.	35
STUDY ON THE DAILY DRIFT BEHAVIOR OF MACROINVERTEBRATE IN THE XIANGXI RIVER	DU Y., ZHANG Y.H., ZHU X., ZHANG M., YANG G.F., QU X.D.	36
A HISTORICAL REVIEW ON MOSQUITO CONTROL RESEARCH IN VIETNAM	DUONG V.C., KIM W.G., SAREEIN N., KIM J.S., NGUYEN V.V., BAE Y.J.	37
METACOMMUNITY STRUCTURE AND ASSEMBLY MECHANISM OF MACROINVERTEBRATE AND DIATOM WITHIN THREE INTERMEDIATE STREAM NETWORKS LOCATED AT DIFFERENT GEOGRAPHIES	HE S.W., CHEN K., RAJPER A.R., DING N., WANG B.X.	38
MULTIPLE FACETS OF STREAM MACROINVERTEBRATE ALPHA DIVERSITY ARE DRIVEN BY DIFFERENT ECOLOGICAL FACTORS ACROSS AN EXTENSIVE ALTITUDINAL GRADIENT	LI Z.F., JIANG X.M., WANG J., MENG X.L., HEINO J., XIE Z.C.	39
COMMUNITY STRUCTURE OF MOLLUSCS AND THEIR RELATIONSHIP WITH ENVIRONMENTAL FACTORS IN SOUTH DONGTING LAKE	LIU Z.Y.	40
THE IMPACT OF URBANIZATION ON DIATOM COMMUNITY STRUCTURE IN QIANTANG RIVER WATERSHED, CHINA	MBAO E., CHEN K., GAO J., WANG Y., WU C., HU Y.L., SITOKI L., OMONDI S., WANG B.X.	41
RESPONSES OF MACROINVERTEBRATES AND LOCAL ENVIRONMENT TO SHORT-TERM COMMERCIAL SAND DREDGING PRACTICES IN A FLOOD-PLAIN LAKE	MENG X.L., JIANG X.M., LI Z.F., WANG J., COOPER K.M., XIE Z.C.	42
PHYTOPLANKTON OF THE MIDDLE PART OF THE AMUR RIVER: SPECIES DIVERSITY, DOMINANT'S CHANGE AND QUANTITATIVE CHARACTERISTICS IN THE SUMMER PERIOD	NIKULINA T.V.	43
WEATHER, LAND COVER AND ANTHROPOGENIC IMPACT ON MOSQUITO POPULATION DYNAMICS IN CHIANG MAI CITY, THAILAND	RAHONG P., TECHAKIJVEJ C., SAREEIN N., BAE Y.J., PHALARAKSH C.	44
EFFECTS OF FLOOD DISTURBANCE ON COHORT STRUCTURE OF RIVERINE MAYFLY *EPHEMERA ORIENTALIS* (EPHEMEROPTERA: EPHERMERIDAE) IN THE HAN RIVER IN SEOUL, KOREA	SEOK S.W., BAEK M.J., HWANG J.M., PARK S.H., BAE Y.J.	45
METACOMMUNITY STRUCTURE OF BENTHIC MACROINVERTEBRATES VARIES BETWEEN AUTUMN AND WINTER IN POYANG LAKE CATCHMENT	TAN C.Z., WU C., GAO J., FU R., WANG B.X.	46
DIVERSITY OF BENTHOS IN GANJIANG RIVER AND ITS CORRELATION WITH ENVIRONMENTAL FACTORS	XING Y., XIE Z.C.	47
RELATIONSHIP BETWEEN MACROPHYTE COMMUNITIES AND MACROINVERTEBRATE COMMUNITIES IN AN URBAN STREAM	YU Y., QU X.D., ZHANG M., ZHANG H.P.	48

POSTER SESSION

Title	Authors	Page
S01: Asian Freshwater Biomonitoring and Bioassessment: Methods, Perspectives and Challenges		
METACOMMUNITY ECOLOGY MEETS BIOASSESSMENT: ASSESSING SPATIO-TEMPORAL VARIATION IN MULTIPLE FACETS OF MACROINVERTEBRATE DIVERSITY IN HUMAN-INFLUENCED LARGE LAKES	CAI Y.J., ZHANG Y., HU Z.X., DENG J.M., QIN B.Q., YIN H.B., GONG Z.J., WANG X.L., HEINO J.	51
SPECIES DETECTION PERFORMANCE OF MACROINVERTEBRATES USING ENVIRONMENTAL DNA METABARCODING BETWEEN WATER SAMPLES AND ETHANOL SAMPLES	WANG Y., WANG B.X., GAO J.	52
MACROINVERTEBRATE BIODIVERSITY IN RELATION TO ENVIRONMENTAL VARIABLES OF LITTORAL ZONE IN THE LOWER YANGTZE RIVER FROM NANJING TO THE ESTUARY	WU C., XU J., YIN S.L., TAN C.Z., CHEN K., GAO J., WANG B.X.	53
IMPROVING THE MACROINVERTEBRATE-BASED BI CLASSIFICATION CRITERIA FOR WATER QUALITY ASSESSMENT IN ZHENGJIANG PROVINCE, EASTERN CHINA	ZHANG J.W., CHEN K., HE S.W., WANG B.X.	54
S02: Benthos Biodiversity Conservation and Rehabilitation		
SOME DATA ABOUT MACROZOOBENTHOS IN LITTORAL ZONE OF ARCTIC LAKES OF THE PUTORANA PLATEAU, KRASNOYARSK REGION, RUSSIA	BAZHINA L.V., SEMENCHENKO K.A., KLEUSH V.O.	55
DISTRIBUTION OF DECAPOD CRUSTACEANS IN THE TRUONG GIANG RIVER, QUANG NAM PROVINCE, VIETNAM	NGO X.N., NGUYEN N.H., NGUYEN V.V.	56
SPECIES DIVERSITY OF PERYPHYTON ALGAE FROM THE GASSI LAKE (THE LOW AMUR RIVER, RUSSIA)	NIKULINA T.V.	57
SEASONAL DYNAMICS OF MACROINVERTEBRATE COMMUNITY STRUCURE IN A HEADWATER STREAM IN THE CHANGBAI MOUNTAINS	WANG L., YANG H.J., LIN C.L., CHEN G., LIU Y.W., GONG Y.W., TAN Y.	58
S03: Impacts on Community Structure and Function		
EFFECTS OF HUMAN ACTIVITIES ON MACROZOOBENTHOS IN GUAN RIVER BASIN OF DANJIANGKOU RESERVOIR AREA	HAN X.M., YANG X.M., GUO S.J., LI Y.Y.	59
BENTHIC MACROINVERTEBRATE COMMUNITY DISTRIBUTION IN RESERVOIR AND UNDER DAM OF YULIANG SHIPPING HUB IN YOU RIVER GUANGXI PROVINCE	WANG H.L., LI H.T., LI N., TAO M., ZHANG H.W., WANG Q., XU X., ZHANG Q.H., SHU S.	60
S04: Taxonomy, Evolution, and Systematics		
CONSTRUCTION OF REGIONAL DNA BARCODE LIBRARY OF MOLLUSCA IN YANGTZE RIVER DELTA	FU R., WANG B.X., CHEN K.	61
DESCRIPTIONS OF LARVAE OF FIVE PHILOPOTAMIDAE SPECIES FROM CHINA (INSECTS, TRICHOPTERA)	HU Y.L., WANG B.X., SUN C.H., PENG L., WANG Y.	62
TWO NEW RECORDS OF LEUCTRIDAE (PLECOPERA) FROM SOUTH KOREA	HWANG J.M., MURANYI D., KANG J.H., SEOK S.W., PARK S.W.	63
THE GENUS *PSEUDONEURECLIPSIS* ULMER (PSEUDONEURECLIPSIDAE, TRICHOPTERA) IN JAPAN	INABA S., NOZAKI T.	64

Title	Authors	Page
NOTES ON FIVE MICROCADDISFLIES (TRICHOPTERA: HYDROPTILIDAE) RECORDED FOR JAPAN, ONE A NEW DESCRIBED SPECIES	ITO T., SHIMURA N.	65
A MYSTERIOUS REALM OF ANIMALS HIDDEN IN CAVE: AN INTRODUCTION TO THE TROGLOFAUNA	JIANG X.K., XIE Z.C.	66
THE GENETIC STRUCTURE AND THE MOLECULAR PHYLOGEOGRAPHY OF *EPHEMERA* MAYFLIES	KOGAWARA H., TAKENAKA M., TOJO K.	67
STRUCTURAL CHARACTERISTICS OF CHIRONOMID COMMUNITY AND THEIR INDICATIVE SIGNIFICANCE IN BIOASSESSMENT OF WATER QUALITY IN YONGAN RIVER OF XIANJV, ZHEJIANG	LI Y.L., KONG Q.Q., ZHANG R.L., QI X.	68
DESCRIPTIONS OF FIVE NEW SPECIES OF THE GENUS *HOMOPLECTRA* (TRICHOPTERA, HYDROPSYCHIDAE) FROM JAPAN WITH REASSIGNMENT OF *HOMOPLECTRA TOHOKUENSIS* (KOBAYASHI, 1973)	NOZAKI T.	69
HISTORICAL REVIEW AND AN AMENDED CHECKLIST OF TRICHOPTERA (INSECTA) OF THE KOREAN PENINSULA	PARK S.J., KONG D.	70
GLOCHIDIA MORPHOLOGY OF SOME ASIAN MOLLUSCS (BIVALVIA, UNIONIDAE)	SAYENKO E.M.	71
COMPREHENSIVE DNA BARCODES FOR SPECIES IDENTIFICATION AND DISCOVERY OF CRYPTIC DIVERSITY IN MAYFLY LARVAE FROM SOUTH KOREA	SUH K.I., HWANG J.M., BAE Y.J., KANG J.H.	72
PRELIMINARY STUDY ON DIVERSITY OF WHIRLIGIG BEETLES (COLEOPTERA: GYRINIDAE) IN NORTHERN THAILAND	SUKSAI B., SANGPRADUB N.	73
AN UPDATE TO THE TRICHOPTERA FAUNA OF SOUTH KOREA WITH A REPORT OF NEW RECORD	UY CHRISTINE J. C., SAREEIN N., DUONG V.C., BAE Y.J.	74
A REDESCRIPTION OF *CHIRONOMUS (CHIRONOMUS) FLAVIPLUMUS* TOKUNAGA (DIPTERA: CHIRONOMIDAE) FROM CHINA	ZHANG R.L., ZHOU D., CHEN S.	75
S05: Population, Assemblage, and Community Ecology		
BIODIVERSITY AND DISTRIBUTION OF EPHEMEROPTERA, PLECOPTERA AND TRICHOPTERA ALONG LONGITUDINAL ZONES OF THE KHE STREAM, QUANG NAM PROVINCE, VIETNAM	DUONG V.C., NGO X.N., NGUYEN V.V., BAE Y.J.	76
DIVERSITY OF TASTE PREFERENCES IN BENTHIVOROUS CARP FISHES	ISAEVA O.M., KASUMYAN A.O.	77
TRICHOPTERA TAXONOMY AND FAUNA OF DABIE MOUNTAINS	QIU S., YAN Y.J.	78
SCALE EFFECTS ON ELEVATIONAL PATTERNS OF TAXONOMIC RICHNESS AND FUNCTIONAL DIVERSITY OF AQUATIC INSECTS IN THE UPPER LANCANG-MEKONG BASIN	WEI H.Y., CHEN K., WANG B.X., DING N., CHEN Q.W.	79

ORAL SESSION

ABSTRACTS

Oral Session S01

INCORPORATING TRAIT AND FUNCTIONAL DIVERSITY TO ENHANCE MULTIMETRIC INDEX PERFORMANCE AND ASSESS LAND USE GRADIENTS

K. Chen[1], R.M. Hughes[2], J.R. Olson[3], B.X. Wang[1]
[1] Department of Entomology, Nanjing Agricultural University, Nanjing, Jiangsu 210095 P.R. China
[2] Amnis Opes Institute and Department of Fisheries and Wildlife, Oregon State University, Corvallis, Oregon 97333, USA
[3] School of Natural Sciences, California State University Monterey Bay, Seaside, California 93955 USA

Trait information has proven useful for characterizing ecosystem function and structure, detecting and providing mechanistic explanations for environmental changes, and assessing ecological integrity. However, the practice and application of aquatic insect trait composition and functional diversity are infrequently included in multimetrics indices (MMIs) for stream and river bioassessment. We sampled 90 stream sites in eastern China to incorporate diversity and functional trait metrics into a regional site-specific, model-based, predictive MMI (pMMI) which can assess the integrity of aquatic insect assemblages and their diagnose causes of impairment. Our final pMMI summed 5 scaled metrics describing different aspects of macroinvertebrate assemblage characteristics: functional richness, Rao's Quadratic Entropy, frequency of soft body occurrence, frequency of predator occurrence, and number of Diptera taxa. The natural variation explained within the metrics ranged between 19.62% and 71.02%, indicating that taxa and trait composition and functional diversity changed systematically along natural environmental gradients. The pMMI clearly distinguished the least-disturbed sites from the most-disturbed sites, exhibited high precision and low bias, and showed a significant negative response to anthropogenic stressors. Functional richness, Rao's Quadratic Entropy, and frequency of predator occurrence were generally lower at most-disturbed sites than at least-disturbed sites, but frequency of soft body occurrence increased at intermediate and most-disturbed sites. The pMMI and its metrics responded nearly linearly from least-disturbed to intermediate sites, but responded less markedly from intermediate to most-disturbed intensities of land use. The response of pMMI decrease along percent urban and agriculture at threshold of 0.08 and 0.17, while threshold of non-trait information based pMMI were at 0.08 and 0.22. These findings suggest that our pMMI is an effective indicator for assessing ecological condition and for determining how human pressures modify the function and structure of macroinvertebrate assemblages, thereby improving our predictive capability regarding patterns and processes in freshwater ecosystems.

Key words: biological traits, functional diversity, MMI, aquatic insects, land use, bioassessment

METABARCODING BASED MACROINVERTEBRATE COMMUNITY ASSESSMENT UNDER THE INFLUENCE OF ARTIFICIAL GRAVEL BARS IN THE DOWNSTREAM OF DAM IN TRINITY RIVER

B. Li.[1], J. S[1], T. S[2], Y. T[2], K. W[1]
[1] Department of Civil and Environmental Engineering, Ehime University, Bunkyo-cho 3 Matsuyama, Ehime Prefecture, Japan
[2] Disaster Prevention Research Institute, Kyoto University, Uji Kyoto, Japan

Dam construction obstructed migration pathways of organism and trapped sediment which brought many adverse effect on the ecosystem in the downstream of the dam. In-channel gravel features such as gravel bars are artificially created in the main river channel which play important ecological roles in rivers under the influence of dam. The Trinity River Restoration Program aims to restore the Trinity River channel by combining stream regimen and sediment control in the downstream of Lewiston dam to maintain or increase ecosystem services while protecting downstream ecosystems. The addition of coarse sediment downstream aims to mitigate sediment starvation, reestablishing normative rates and magnitudes of physicochemical and biological processes and rebuilding geomorphic structures required for restoration of ecological functions. In order to evaluate the restoration performance of artificial gravel bars, we investigated the macroinvertebrate community and biodiversity using Throughput Sequencing (HTS) technologies and assess the water quality purification function of the artificial gravel bars by comparing water quality in bar head and tail in Trinity River downstream of the Lewiston Dam. The influence of gravel bars on macroinvertebrate community will also be studied.

Key words: macroinvertebrate, gravel bar, next generation sequencing, water quality, dam

DEVELOPMENT AND APPLICATION OF A MACROINVERTEBRATE-BASED INDEX OF BIOTIC INTEGRITY IN NORTHERN RIVER OF CHINA: A CASE STUDY OF SONGHUA RIVER

K.X. Lin, L. Li, L.S. Liu, Y.L. Liu
Chinese Research Academy of Environmental Sciences, No.8 Dayangfang Street, Chaoyang District, Beijing, China

Benthic macroinvertebrate based Index of Biotic Integrity (B-IBI) was developed to assess the health condition of Songhua River Basin. Macroinvertebrate communities were sampled at 37 sites of Songhua River in June and September, 2016. Among the 28 candidate biological metrics, totally 5 core metrics were selected to construct B-IBI, including total number of taxa, number of Chironomid taxa, relative abundance of sensitive taxa, Hilsenhoff Biotic Index (HBI), Marglef richness index. The B-IBI scores were calculated by 0-10 ratio scoring method. The results indicated that 60% of sites showed different degree of degradation in Songhua River Basin. Moreover, B-IBI could reflect macroinvertebrate communities condition, physical habitat quality and chemical water quality synthetically.

Key words: River Ecosystem, Benthic Macroinvertebrate, Index of Biotic Integrity, Health Assessment, Songhua River

THE APPLICABILITY ASSESSMENT OF CANDIDATE AQUATIC SPECIES USED TO ONLINE BEHAVIOURAL MONITORING BASED ON QUANTITATIVE ION CHARACTER-ACTIVITY RELATIONSHIPS (QICARS) AND EXPERIMENTAL EXPOSURES TO HEAVY METHALS

Y.D. Liu[1], H. Wang[1], Z.Y. Liu[1], X.L. Chen[1], F.C. Wu[2], J.P. Giesy[3]

[1] The Key Laboratory of Water and Air Pollution Control of Guangdong Province, South China Institute of Environmental Sciences, Guangzhou 510065, P.R. China
[2] State Key Laboratory of Environmental Criteria and Risk Assessment, Chinese Research Academy of Environmental Sciences, Beijing 100012, P.R. China
[3] Department of Veterinary Biomedical Sciences and Toxicology Centre, University of Saskatchewan, Saskatoon, SK, Canada

As a biological indicator, aquatic animal behavior could efficiently reflect the impacts of water quality changes on their heath conditions. It has a prospective application on the water quality monitoring and aquatic environmental protection, in terms of the importance on real time monitoring and alarming function in case sudden water pollution accidents occur. Firstly, several typical heavy metals (Cd, Cr, Cu, Hg, Ni, Pb, Sb and Zn) those have ever caused serious water pollutions in the past decade were selected to test movement behaviors of aquatic species, and create prediction models, based on quantitative ion character-activity relationships (QICARs) and biological abilities. Toxicity data on behaviors and other biological effects (i.e., LC50) were further predicted through QCAIRs models respectively, once the QCARIs models were verified to be accurate and robust enough. The predicted behavioral and general toxicity data, in combination with those obtained from databases and experimental tests, were analyzed to study the relationships in between them based on the structure parameters of heavy metals, and the applicability of candidate aquatic species used to online behavioral monitoring was assessed subsequently. Finally, the suitable species list was provided as a screening tool for behavioral monitoring in water environments. In addition, an environmental threat model was established based on the relationships of heavy metals exposure - structure parameters – behavioral responses, and to theoretically support the future establishment of an integrative online monitoring system, including species and pollutants screening, data extraction, data analysis and online alarming function.

Key words: heavy metal, movement behavior, aquatic species, QICARs, biological monitoring

USE OF AQUATIC INSECTS AS BIOINDICATORS OF WATER QUALITY IN KWAN PHAYAO, PHAYAO PROVINCE, NORTHERN THAILAND

K. Phosanga[1], B. Jaitrong[1], C. Jitmanee[1,2]
[1] Demonstration School, University of Phayao, Phayao 56000, Thailand
[2] Division of Environmental Science, School of Energy and Environment, University of Phayao, Phayao 56000, Thailand

Kwan Phayao is a large freshwater lake in Muang district, Phayao province, Northern Thailand what is an important for survival of the Phayao population because Kwan Phayao is covers a wide area, including amount of the use of the community. Kwan Phayao affected by the contamination of waste from human activities, that affect the creatures that live in this area and reducing of habitat or loss of habitats affects for several organism biodiversity.

The use of aquatic insects as bioindicators of water quality in Kwan Phayao has conducted in 6 times during May 2017 to March 2018. The sample of aquatic insects and physico-chemical properties of water have collected from 8 study sites around Kwan Phayao. The aquatic insect samples have collected with 3 replicates from each site by using pond net. Diversity index and ASPT were used to analyze aquatic insect data. Physico-chemical properties were measured to compare with the surface water quality standard of Thailand. 7 orders and 34 families were recorded. The most abundant family was Libellulidae in Odonata order, Caenidae in Ephemeroptera order, and Baetidae in Ephemeroptera order respectively. The values of average score per taxa (ASPT) and diversity index were evaluated. The average values of ASPT ranged from 3.50 - 6.63 and the values of diversity index ranged from 1.19 – 3.27. The results indicated that water quality was moderate to quite dirty. The water quality from physico-chemical properties and the use of aquatic insects as bioindicators of water quality were found in the same results. The physico-chemical properties of water from all sampling sites were in the CLASS 3-4 when compare with standard for surface water quality of Thailand, depending on agriculture, water transport, industrial and consume when passed sterilize. According to cluster analysis method resulting that the water quality data from the study sites were clustered into 5 groups, related to season, conductivity and TDS.

Key words: water quality, aquatic insects, biodiversity, Kwan Phayao

FLUCTUATING ASYMMETRY IN POLLUTION-TOLERANT CADDISFLY *HYDROPSYCHE DOCTERSI* AS AN INDICATOR OF RIVER CONDITION

A.H. Suhaila, M.A. Mohd Fakhrullah Salafusalam
School of Biological Sciences, Universiti Sains Malaysia, 11800 Minden, Penang, MALAYSIA

In biomonitoring program, understanding the responses and effects of aquatic insect communities and ecosystem themselves towards pollution and environmental stressor are vital, which later may help in bioassessment of water quality. Aquatic insect has good potential to be used as the bioindicators in monitoring the 'health' status of rivers and streams. It is more accurate to investigate the effect of pollution or land use activities at low organization levels of organism that is by using single individual. Changes in certain biological traits and morphological deformations has been used as the benchmarks in the study of environmental effects towards certain organisms. The morphological deformities in aquatic insect such as fluctuation asymmetry or FA is measured in any living organism has been proposed as a reliable index of genetic or environmental health. In this study, several morphological traits of *Hyropsyche doctersi* 5th instar larvae were studied and measured. FA11 was noted in 3rd femur length, 2nd tibial width, 1st tibial length and mesonotum length of *Hydropsyche doctersi*. Five out of thirteen traits recorded from *Hydropsyche doctersi* shows FA from the selected rivers. The greatest level of FA11 was noted in 3rd femur length of the *Hydropsyche doctersi*. Present study shows the correlation of some water chemical parameters with the FA descriptors (AbsFA and sign FA) and FA index (FA11) in some traits. The high level of certain water chemical parameters such as nitrate, could possibly altered the fitness of *Hydropsyche* larvae during the ontogeny which later might gave effects on the survival of this species in future. The present study offered such an opportunity to assess the influence of environmental parameters that could stresses the aquatic insects under field investigations.

Key words: bioindicator, river, Trichoptera

THE USE OF BENTHIC MACROINVERTEBRATES AS BIOINDICATORS FOR EVALUATING OF WATER QUALITY OF RIVERS IN RAINY SEASON, THAILAND

C. Techakijvej[1], C. Phalaraksh[1,2]
[1] Environmental Science Program, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand
[2] Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand

Nowadays, the quality of rivers in Thailand has been dramatically changed by many anthropogenic disturbances such as agricultural activities, urbanization and industries. In Thailand, standard water quality is based on chemical measurements, which are not reflected cumulative stressors. Use of benthic macroinvertebrate as bioindicator can reflect overall streams and rivers ecological. The aim of this research is to determine the water quality of the river, and to investigate the environmental quality and the applicability of both the Biological Monitoring Working Party ($BMWP^{Thai}$) and Average Score Per Taxon indices in rainy season. In total, study 32 sites of 14 rivers in Thailand were sampled during late of rainy season (October to November 2017). Physicochemical variables and benthic macroinvertebrate indices were analyzed. As a result, a total of 130 taxa were detected: 99 taxa from Insecta, 16 taxa from Gastropoda, 8 taxa from Bivalvia, 4 taxa from Crustacea, 1 taxa from Oligochaeta, 1 taxa from Hirudinea, 1 taxa from Ostracoda. The water quality of 14 rivers was found to be fair/very poor according to the physicochemical data and good-fair/fair-poor according to the $BMWP^{Thai}$ and ASPT. High biochemical oxygen demand (BOD) and low dissolved oxygen (DO) were the influent factor of physicochemical water quality. However, the water quality from the $BMWP^{Thai}$ and ASPT were different from physicochemical because high water discharges in rainy season. The results suggest that there is still a need for much investigation and testing of the effectiveness of the $BMWP^{Thai}$ and ASPT indices for evaluating of water quality of rivers in Thailand.

Key words: BMWP, benthic macroinvertebrate, Biotic Indices, water quality

THE ASSESSMENT OF LARGE RIVER HEALTH USING BENTHIC-INDEX OF BIOTIC INTEGRITY — A CASE STUDY IN DONGJIANG RIVER OF THE PEARL BASIN

J.Y. Wu[1,2], Z.H. Peng[1,2], H.Z. Wang[1], Y.D. Cui[1]
[1] State Key Laboratory of Freshwater Ecology and Biotechnology, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan 430072, China
[2] University of Chinese Academy of Sciences, Beijing 100049, China

Benthic-Index of Biotic Integrity is one of the most widely used indicators of water ecosystem health assessment. Most of the studies were focused on wading streams, but few studies on large rivers. The Dongjiang River, which is one of the three major tributaries of the Pearl Basin with a watershed area of 35,340 km^2 and a total length of 562 km, was divided into wading and non-wading sections for building B-IBI evaluation system. In normal flow period, benthic macroinvertebrates were sampled in 65 sites in Dongjiang River. We evaluated the ecological health of Dongjiang River with the Benthic-Index of Biotic Integrity (B-IBI). The range of index value distribution, judgment ability and Pearson correlation were analyzed on 32 candidate metrics. Five biological metrics including total number of taxa, percentage of 3 dominant taxa, number of sensitive taxa, individual percentage of tolerant group and number of collector were selected for establishing B-IBI in wading sections. And another five biological metrics including total number of taxa, number of EPT taxa, percentage of Ephemeroptera number, number of sensitive taxa and BI index were selected for establishing B-IBI in non-wading sections. The values of metric were calculated by ratio scoring: the 25% percentile of B-IBI value in reference sites was used to determine the criteria of health ranking, and the distribution range below 25% percentile was divided into 4 quarters. The criterion for the benthic macro-invertebrate is B-IBI＞2.83, 2.13-2.83, 2.13-2.83, 1.42-2.83, 0.71-1.42, 0-0.71 in wading sections and B-IBI＞2.87, 2.16-2.87, 1.44-2.16, 0.72-1.44, 0-0.72 in non-wading sections, which are corresponding to health, sub-health, fair, poor and very poor, respectively. According to the established criteria, results showed that 3.85% sites were healthy; 12.31% sites were sub-healthy; 23.85% sites were in fair condition, and 30.77% sites were in poor and very poor condition. Overall, the assessment of the B-IBI for the Dongjiang River suggested that the environment in the head waters and upper stream were in healthy conditions; however, in the lower reaches, water quality deteriorated seriously.

Key words: Macrozoobenthos, Benthic-index of Biotic Integrity, Health Assessment, Dongjiang River

Oral Session S02

STUDY ON CONSERVATION OF FRESHWATER MOLLUSCA DIVERSITY IN THE YANGTZE RIVER BASIN ON MAXENT MODEL

Y.J. He[1,2], H.Z. Wang[1], Y.D. Cui[1], F.Y. Shu[3], H.J. Wang[1]
[1] State Key Laboratory of Freshwater Ecology and Biotechnology, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan 430072, China
[2] University of Chinese Academy of Sciences, Beijing 100049, China
[3] College of Life Sciences, Qufu Normal University, Qufu 273165, China

Understanding the distribution pattern of target species and its relationship with environmental variables is primary for biological conversation. Recognizing the Yangtze River Basin and its integrity of ecosystem has been facing multiple stressors for decades, the study selected freshwater Mollusca, an ideal and important indicator, as the target conservation group. Three taxonomy groups (Prosobranchia, Pulmonata and Bivalvia) were separated based on the differences of their habitat requirement. In total, distribution data of 318 species were collected from 469 sites and 69 environmental variables were included in the analyses. The suitable habitat and relevant key environmental variables were analyzed by MaxEnt model. The minimum protected area was further simulated according to proportion of endemic species by ArcGIS, to propose conversation advices based on previously established nature reserves for freshwater Mollusca habitat. The results showed that: 1) Topographic and climatic variables were the key factors to explain the distribution variance of Prosobranchia and Bivalvia. Among these variables, elevation, land use, the degree of temperature variation played a primary role. In terms of Pulmonata, the key variables were climate and runoff, among which the degree of temperature and cation exchange capacity of topsoil played a primary role. 2) The suitable habitat area of freshwater Mollusca was estimated at about 250,500 km^2, and the minimum protected area was estimated at about 102,700 km^2. Comparatively, the area of established nature reserves was around 34,000 km^2, being around only 1/3 of the required area. 3) The main distribution locations of freshwater Mollusca are the Poyanghu Lake, the Dongtinghu Lake, the Taihu Lake, and the middle and lower mainstream of the Yangtze River. The distribution of established freshwater ecosystems reserves was relatively narrow and scattered. In consideration of the limited connections between nature reserves, it is suggested to establish an integral conservation network by connecting the scattered reserves.

Key words: freshwater Mollusca, MaxEnt, suitable habitat, minimum protected area, The Yangtze River Basin

BIODIVERSITY OF AQAUTIC INSECTS IN KWAN PHAYAO, PHAYAO PROVINCE, NORTHERN THAILAND

B. Jaitrong[1], K. Phosanga[1], C. Jitmanee[1,2]
[1] Demonstration School, University of Phayao, Phayao 56000, Thailand
[2] Division of Environmental Science, School of Energy and Environment, University of Phayao, Phayao 56000, Thailand

The study of biodiversity of aquatic insects in Kwan Phayao, Phayao province were conducted. Kwan Phayao is a large freshwater lake in Muang district, Phayao province, Northern Thailand where is an important for survival of the Phayao population because Kwan Phayao is covers a wide area, including amount of the use of the community. Kwan Phayao affected by the contamination of waste from human activities, that affect the creatures that live in this area and reducing of habitat or loss of habitats affects for several organism biodiversity. The samples were taking in 3 replicates using the pond net from 8 sampling sites during on May 2017 to March 2018. Shannon-Wiener index and evenness were used to assess species diversity of aquatic insects. Physico-chemical properties were measured to compare with the surface water quality standard of Thailand. Results show that 34 families belong to 7 orders of aquatic insect were identified. The most abundant order was Odonata (7 families), while Lepidoptera (2 families) and Trichoptera (2 families) were the less abundant orders. The dominant family that found in almost study sites were Libellulidae, Caenidae and Baetidae. The most abundant of aquatic insects (7 orders and 24 families) were found from site KW7 in summer. Diversity index were analyzed, site KW2 was the highest values that was 3.27 in rainy, relating less than disturbed sites and found more riparian plant, and site KW7 was the lowest values that was 1.19 relating disturbed from human activity around the study site in winter season. Physico-chemical properties from the study sites were compared, it can be concluded that all sampling sites were shown to standard for surface water quality CLASS 3-4, depending on human activities. The water can use for agriculture and consume when improve the water quality.

Key words: aquatic insects, biodiversity, Kwan Phayao

INITIAL ESTABLISHMENT OF ROUTING MONITORING AND ASSESSMENT METHODS FOR ECOLOGICAL DREDGING EFFECTS ON MACROINVERTEBRATE COMMUNITY IN TAIHU LAKE

H.M. Lu[1], J.B. Wu[2], B.X. Wang[3], L.M. Chen[1], X.H. Li[1]
[1] Nanjing Hydraulic Research Institute, State Key Laboratory of Hydrology-Water Resources and Hydraulic Engineering, Nanjing 210029, P.R. China
[2] Bureau of Wujiang water resources, District of Wujiang, Suzhou 215200, P.R. China
[3] Department of Entomology, Nanjing Agricultural University, Nanjing 210095 P.R. China

Ecological balance between sediment and overlying water could be altered due to the implementation of dredging project, thus the assessment of ecological dredging effects on aquatic ecology in a scientific and sound way has caused widespread concern. However, now such monitoring and assessment methods are absent. Parts of Taihu Lake, including Zhushan Bay, Meiliang Bay and East Taihu, were selected as the representative research area. Macroinvertebrate population was monitored between the year of 2013 and 2015 before and after the implementation of ecological dredging projects. Sampling sites, times and frequency were optimized. Assessing indexes and indicator species were screened out.

Monitoring sites in the dredging area of Zhushan Bay and Meiliang Bay could be optimized into five and two sites respectively using cluster analysis. Routing monitoring on macroinvertebrate population could sample once in the wet and dry season respectively. Based on the variation of macroinvertebrate community, and considering the practical perspective, Wright index, Shannon-wiener biodiversity index, BI index and BPI index were screened out from 34 candidate biological indexes. Six antifouling species including *Glyptotendipes*, *Cricotopus*, *Limnodrilus*, *Branchiura sowerbyi*, *Helobdella* and *Nephthydidae* were selected as indicator species. Routing monitoring and assessment methods for ecological dredging effects on macroinvertebrate community in Taihu Lake were established initially.

Key words: routing monitoring and assessment, ecological dredging, aquatic ecology, sediment, macroinvertebrate, macrophyte, Taihu Lake

GENETIC CHARACTERISTICS OF THE ASIAN GIANT WATER BUGS, *LETHOCERUS DEYROLLEI* AND *L. INDICUS* (HEMIPTERA: BELOSTOMATIDAE) IN ASSOCIATION WITH ARTIFICIAL LIGHT

N. Sareein[1], J.H. Kang[2], T.J. Yoon[2], C. Phalaraksh[2], Y.J. Bae[1]
[1] Department Environmental Science and Ecological Engineering, Korea University, Seoul 02841, Korea
[2] Korean Entomological Institute, College of Life Sciences and Biotechnology, Korea University, Seoul 02841, Korea
[3] Department of Biology, Faculty of Science, Chiang Mai University,Chiang Mai 50200, Thailand

The giant water bugs *Lethocerus* (Hemiptera: Belostomatidae) are the world's largest aquatic insects (around 60–80 mm in body length) and have a global distribution. They are often top predators in shallow standing waters, such as wetlands and paddy fields. Two species, *L. deyrollei* and *L. indicus*, occur in East Asia. *Lethocerus deyrollei* is known to have a restricted and fragmented distribution in Northeast Asia, whereas *L. indicus* is more widely distributed throughout the Oriental region. In addition to habitat loss, artificial light is known to be a critical factor in the local extinction of *L. deyrollei* in Korea. The tropical giant water bug *L. indicus* is a popular food item and regularly sold in local markets: however, the degree to which it is threatened is yet to be evaluated. Seven Northeast Asian population of *L. deyrollei* (Korea and Japan) and nine Thai population of *L. indicus* were collected, and their genetic diversity were examined using the *COI* gene. The population of *L. indicus* showed greater haplotype diversity than the *L. deyrollei* population and were rare in brightly lit areas. By using comprehensive literature reviews, field data, and genetic characteristics, the study demonstrated the level of threat to the two Asian giant water bugs and related it to the intensity of artificial lights on a national scale, as recorded on a satellite map.

Key words: giant water bugs, *Lethocerus deyrollei*, *Lethocerus indicus*, endangered species, artificial lights

MACROZOOBENTHOS COMMUNITY STRUCTURE AND ENVIRONMENTAL DETERMINANTS OF LIUXI RIVER IN GUANGZHOU

K.S. Yao[1,2], Y.D. Cui[1]
[1] State Key Laboratory of Freshwater Ecology and Biotechnology, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan 430072, China
[2] University of Chinese Academy of Science, Beijing 100049, China

Macrozoobenthos community structure of Liuxi River in Guangzhou was investigated in April (normal flow period) and July (high flow period) and November (low flow period). A total of 133 species belonging to 55 families and 127 genera were recorded. Results showed that temporal and spatial variations of the macrozoobenthos community structure were obvious in the Liuxi River. Consequently, the number of species showed a steady decreasing trend from the upper reaches to the lower reaches. The mean density and biomass of macrozoobenthos were 213 ind. /m^2 and 20.02 g/m^2, respectively. The density of oligochaetes and aquatic insects were on predominance, and the biomass of mollusks was on predominance. The density of macrozoobenthos in branches was significantly higher than that in main stem, while the biomass was significantly lower than that in main stem. Temporally, the density was highest in normal flow period, and then higher in low flow period and high flow period. The trend of the biomass distribution was similar in seasons. The Shannon-Wiener index and Margalef index in main stem were lower than those in branches, the Pielou evenness index in the branches was constantly higher than that in main stem, which showed that the community structure of macrozoobenthos in branches was more diversiform and stable than that in main stem. According to the biodiversity index, the lower reaches of Liuxi River was polluted to a certain extent and the main stem was more serious. Redundancy analysis showed that organic matter, total phosphorus and dissolved oxygen were strongly correlated with the macrozoobenths community structure.

Key words: macrozoobenthos, community structure, redundancy analysis, Liuxi River

Oral Session | S03

TRAITS UNDERDISPERSION AND OVERDISPERSIOIN OF BENTHIC MACROINVERTEBRATE IN THREE CHINESE WATERSHEDS ACROSS TROPICAL TO SUB-TROPICAL REGIONS AND THE EFFECT OF ENVIRONMENTAL CONSTRAINTS

N. Ding[1,2], B.X. Wang[1], J.H.C. Cornelissen[2], M.P. Berg[3], K. Chen[1]
[1] Department of Entomology, Nanjing Agricultural University, Nanjing 210095 P.R. China
[2] Systems Ecology, Department of Ecological Science, Faculty of Sciences, VU University, Amsterdam, The Netherlands
[3] Department of Ecology Science, Section Animal Ecology, VU University Amsterdam, Amsterdam 1081 HV, The Netherlands

Understanding the different processes structuring the community composition remains a key challenge for ecologists. Environmental filtering, dispersion and competition have frequently been considered to decide whether and how species can assemble into local communities from the regional species pool. In terms of these processes, environmental filtering and dispersion lead to species being more similar (underdispersion) than expected from a random distribution. On the contrary, competition may lead species being more different (overdispersion), which suggests niche partitioning. Most previous studies on community assembly based on species occurrences or abundances just focus on part of these processes (environmental filter, dispersion or competition) or can only detect one of those two patterns (underdispersion or overdispersion). However, it is likely that multiple factors will influence community assembly simultaneously. Thus, it is important to understand, under which conditions, each process predominates and what the pattern may actually be. More importantly, because of different importance of these processes under changing conditions, how about the relationships between underdispersion and overdispersion? We sampled benthic macroinvertebrate species from multiple watersheds in each of three different regions (Zhejiang, Xian and Yunnan province) with different human disturbance and collected data of their key functional traits with respect to environmental tolerances, dispersal ability and competitiveness. The analysis was performed using a functional diversity index (Rao's quadratic entropy) in combination with a null model approach on functional traits. pRDA was used to test the contribution of environmental or spatial factors to different groups of traits in different regions. Additionally, we examined the correlations between body size (reflect the competitive trait) and all the dispersal traits. We found that: 1) environmental filtering dominates the trait changes of macroinvertebrates in disturbed conditions, but competition plays an more important role in the least disturbed conditions, 2) communities with weak dispersal ability may be more limited by spatial factors than communities with strong dispersal ability and 3) body size (competitive traits) of predators are positively correlated with dispersal traits across species, but non-predators are negatively correlated with dispersal traits.

Key words: environmental filter, dispersion, competition, disturbance

SENSITIVE TRAITS AND TRAITS COMBINATIONS REVEAL THE FUNCTIONAL DIVERSITY DECLINE OF STREAM MACROINVERTEBRATE ASSEMBLAGES IN RESPONSE TO URBANIZATION

J. Gao, B.X. Wang, K. Chen, A.R. Rajper
Department of Entomology, Nanjing Agricultural University, Nanjing 210095 P.R. China

Species and functional diversity losses are the core concern of community ecology and biodiversity conservation. The loss of sensitive functional trait categories and the local extinction of sensitive species owning combinations of specific trait categories were possible mechanisms to the community functional diversity decline. The functional diversity of stream macroinvertebrates has widely declined due to the rapid land use changes in Yangtze River delta in the past three decades. Here, we aimed to identify the single trait category and the combinations of trait categories sensitive to the impact of urbanization, respectively.

The data of macroinvertebrate and relevant environmental indicators were collected from 82 stream sites in Qiantang river basin, Zhejiang, china from 2010 to 2011. We first performed elements of metacommunity structure framework, hierarchical clustering and principal component analysis to identify and verify compartments with different levels of urbanization pressure in the metacommunity. Then, we determined the sensitive trait categories using t-test between two abundance-weighted site-trait frequency matrixes of adjacent compartments. Finally, we performed the classification and regression tree (CART) algorithm to examine the functional trait combinations owned by sensitive species.

Macroinvertebrate metacommunity in urban streams exhibited Clementsian structure composed of three major compartments reflecting low, medium and high levels of urbanization. Compared with the compartment with least anthropogenic pressure, compartments exposed to greater human disturbance had significant lower biodiversity in both species and functional aspects. We identified 12 sensitive trait categories, such as building shelters with leaf parts or wood and branchial respiration, from low to medium level of urbanization (U_{LM}), and the frequency of 11 sensitive categories, such as sprawlers, swimmers and gatherers, remarkably declined from medium to high level of urbanization (U_{MH}). The CART showed species with trait category conjunction of filterers or predators and burrows or swimmers at the U_{LM} process, and non-integumentary inspirators at U_{MH} process were more vulnerable than species with other jointed trait category or trait category, respectively. Our results demonstrated the lost process of traits of macroinvertebrates assemblages along a gradient of urbanization and highlighted the perspective of trait combinations in uncovering the species vulnerable to disturbance and sensitive traits in understanding the degradation of functional diversity.

Key words: trait category, metacommunity structure, compartment, sensitive species, Qiantang river

SECONDARY SUCCESSION OF BENTHIC MACROINVERTEBRATE COMMUNITIES IN THE HAN RIVER IN SEOUL, KOREA

S.H. Park, S.W. Seok, Y.J. Bae
Department of Environmental Science and Ecological Engineering, Korea University, Seoul 02841, Republic of Korea

The Han River, which runs across the Seoul city and divides the city into the north (Gangbuk) and south (Gangnam) Seoul, has been represented the rapid economic growth of the country as referred to “Miracle on The Han River” in the 1960s and 1970s. Since the end of the Korean War (1953), the riverbed of the Han River has been destroyed by dredging for the collection of construction materials as well as by the inflow of domestic sewage. Since the 1980s, the river banks within Seoul city have been channelized, and construction of the overflow weirs have altered stream velocity and the riparian area. In our research, we looked at the correlation between the succession of benthic macroinvertebrates and environmental factors, such as water quality, using long-term data from monitoring of the Han River. To examine the correlation between the benthic macroinvertebrate community and environmental variables, we analyzed datasets from long-term monitoring of the Han River, which was conducted from 1987 to 2017 at approximately five-year intervals (7 times in total). Benthic macroinvertebrates were quantitatively sampled from nine to 31 sites each sampling time along the watercourse using a Surber sampler (50 x 50 cm; mesh 0.25mm, two replications per site). The chemical water quality data were provided by Ministry of Environment of the Republic of Korea. We analyzed the community of benthic macroinvertebrates and water quality using a self-organizing map (SOM), which is a type of artificial neural network. Although there were no available reference data before 1987, species richness of benthic macroinvertebrates in the study area generally increased after 1987, when the channelization was completed, with a peak of 114 species in the year 2001 to 2002. Our analysis of the correlation between the water quality and the composition of benthic macroinvertebrate communities showed that ammoniacal nitrogen (NH_3N), chemical oxygen demand (COD), electrical conductivity, suspended solids, and total nitrogen were correlated with the number of species, dominance index, diversity index, and richness index.

Key words: benthic macroinvertebrates, community succession, Han River, Korea, Self-organizing map

EFFECT OF WATERSHED URBANIZATION ON EPT (EPHEMEROPTERA, PLECOPTERA AND TRICHOPTERA) COMMUNITY IN THE MIDDLE QIANGTANG RIVER BASIN, ZHEJIANG PROVINCE, CHINA

A.R. Rajper, S.W. He, K. Chen, E. Mbao, J.W. Zhang, B.X. Wang
Department of Entomology, Nanjing Agricultural University, Nanjing, 210095, P.R. China

Stream condition is constantly suffering from the increasing urbanization worldwide**.** EPT is a group of aquatic insects sensitive to water pollution and a widely used indicator of stream biodiversity and condition. In this study we examined how EPT richness, EPT abundance and EPT functional group response to urbanization in Qiantang River Basin. Environmental and biological data of 49 sampling sites, located in 22 reference and 27 urban streams, were collected in April to May, 2011 to 2012. Wilcoxon rank-sum test showed that urban streams were of significantly lower %cobbles, %boulders and DO, but higher water temperature, average river width, average wet width, average depth, %pebbles, %silt, TN, NH_4-N, TP, and EC than reference streams. Moreover, urban streams had significantly lower total EPT taxa richness, EPT individuals, %EPT, %intolerant EPT, E taxa richness, T taxa richness, intolerant EPT taxa richness, %scrapers, %shredders and %filterers, however the %collector-gatherers remarkably increased. Spearman correlation analysis revealed that Total EPT taxa richness, EPT individuals, E taxa richness, T taxa richness, intolerant EPT taxa richness, %EPT, %scrapers, %filterers, %shredders and %intolerant EPT were negatively and significantly correlated with WT, average wet width, average depth, TN, TP, COD, %silt, %agriculture and %urban land uses, In addition, EPT richness, intolerant EPT richness, %EPT and most of functional groups were positively and significantly correlated with %cobbles, %boulders %pebbles, DO and %forest, collector-gatherers negatively and significantly associated with %cobbles, %boulders, Do and %forest. Poisson generalized linear model showed richness metrics such as EPT richness, E taxa richness, T taxa richness and intolerant EPT richness were best predicted by %urban, %agriculture land uses and forest% (adjusted r^2>0.9), whereas abundance and functional metrics are less predicted by three land use types (adjusted r^2<0.5). Our results highlighted the EPT as indicator in early warning of urban land use change.

Key words: Land use change, Stream, Macroinvertebrates, Biodiversity, Agricultural land use

SEASONAL VARIATION OF THE IMPACTS OF AGRICULTURE ON MACROINVERTEBRATE FUNCTIONAL TRAITS AND FUNCTIONAL DIVERSITY IN HIGH LATITUDE STREAMS

L. Wang, H.J. Yang, Y.Z. Gao
Key Laboratory of Vegetation Ecology, Northeast Normal University, Changchun, 130024, China

In recent years, studies on macroinvertebrate functional traits and functional diversity have increased year by year, but how they change over time in response to the environment is poorly understood. This study was conducted in a forest stream and an agricultural stream in the Changbai Mountains, China. By using in-situ sampling in the wild, we attempt to elucidate the temporal characteristics of the functional composition of macroinvertebrates, and the effects of agriculture on stream ecosystem. The main conclusions are as follows: (1) The difference in composition of both species and functional traits between the two streams was significant in each season, fitting the expectations of habitat-templet theory. (2) Despite high seasonal variation in species composition, functional traits of macroinvertebrate varied less and exhibited seasonal stability in wet season and normal season, which may be because of the unique habitat constraints of stream environment, regardless of the season. (3) There were varying degrees of relevance between species diversity and functional diversity, and they were generally shown to be lower in the agricultural stream. But there was no difference in functional diversity between the two streams in dry season, which may be a result of the relatively similar habitat environment of the two streams in winter, making by low temperature and freezing. (4) The difference in functional redundancy between the two streams was not significant, indicating that agriculture in the Changbai Mountains has no impact on the functional stability of the stream ecosystem. (5) Total nitrogen, total phosphorus, temperature, turbidity and substrate structure were the main environmental factors affecting the functional composition of the agricultural stream. Our results also indicated that functional metrics could reflect the status of regional environmental in terms of ecosystem function, and they should be widely used for macroinvertebrate biodiversity conservation and monitoring.

Key words: macroinvertebrate, functional composition, agriculture, seasonal variation

EFFECTS OF ANTHROPOGENIC SUBSIDY AND GLYPHOSATE ON MACROINVERTEBRATE ASSEMBLAGES IN STREAMS

H.Y. Xiang[1,2], Y.X. Zhang[1,3,4], D. Atkinson[2], S. Raju[5]
[1] Department of Environmental Science, Xi'an Jiaotong-Liverpool University, Suzhou, China
[2] Institute of Integrative Biology, University of Liverpool, Liverpool, United Kingdom
[3] XJTLU Huai'an Research Institute of New-Type Urbanization, Huai'an, China
[4] XJTLU Suzhou Urban and Environmental Research Institute, Suzhou, China
[5] Department of Biological Sciences, Xi'an Jiaotong-Liverpool University, Suzhou, China

Streams and surrounding terrestrial ecosystems are closely linked by numerous mutual resource subsidies. Also, streams receive many new emerged subsidies such as fishing bait and waste food because of the increased anthropogenic activities. Furthermore, anthropogenic stressors such as herbicide can enter streams through run off. However, the individual and interactive effects of anthropogenic subsidy and herbicide stressor on stream macroinvertebrate assemblages are not fully understood. In this study, we conducted a 2×2 full factorial design in four streams which differ in land use in Huangshan, China. We manipulated anthropogenic subsidy (chicken meat) and stressor (glyphosate) to investigate their individual and combined effects on macroinvertebrates colonizing in coarse leaf bags, and how these effects change with different land use scenario. All the measured macroinvertebrate variables differed between streams. In pristine stream (H4), glyphosate decreased Shannon-Weiner diversity index and predator's proportion, while subsidy elevated insect richness. In light-medium disturbed streams (H2 and H3), subsidy enhanced total species richness, while reduced EPT's (Ephemeroptera, Plecoptera and Tricoptera) proportion. In high anthropogenic disturbed stream (H1), glyphosate enhanced total species richness, Shannon-Weiner diversity index, Simpson's diversity index, insect richness, and collector-gatherer richness. On the contrary, subsidy declined total species richness, Shannon-Weiner diversity index, Simpson's diversity index, insect's abundance and richness, Chironomidae's abundance and proportion, collector-gatherer's richness and proportion, and predator richness, while increased predator's proportion. Collectively, these results imply that anthropogenic activities can mask the effects of anthropogenic subsidy and glyphosate on macroinvertebrates. With increasing level of anthropogenic activities, the effects of subsidy on macroinvertebrates shift from positive to negative, whereas, glyphosate may reverse from its negative effects to positive effects. Therefore, when managing stream ecosystems facing problems of anthropogenic subsidy and glyphosate, we should take different actions according to different anthropogenic activity stress.

Key words: land-water interaction, herbicide, land use, community structure

NUTRIENT ENRICHMENT HOMOGENIZES TAXONOMIC AND FUNCTIONAL DIVERSITY OF BENTHIC MACROINVERTEBRATE ASSEMBLAGES IN SHALLOW LAKES

Y. Zhang[1], L. Cheng[2], K.Y. Li[1,3], L. Zhang[1], Y.J. Cai[1], X.L. Wang[1], J. Heino[4]
[1] Key Laboratory of Watershed Geographic Sciences, Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences, 210008, Nanjing, P.R. China
[2] Nanjing Hydraulic Research Institute, 210029, Nanjing, P. R. China
[3] Sino-Danish College, University of Chinese Academy of Sciences, Beijing 100049, China
[4] Finnish Environment Institute, Biodiversity Centre, Paavo Havaksen Tie 3, FI-90570 Oulu, Finland

Eutrophication alters the trophic dynamics in lakes and may result in biotic homogenization. How nutrient enrichment drives patterns of taxonomic and functional homogenization of macroinvertebrate assemblages at within-lake (local) and among-lakes (regional) scales is, however, not well understood. Taxonomic and functional composition of macroinvertebrate assemblages in 41 lakes of the middle and lower reaches of the Yangtze River and Huaihe River were analyzed at within-lake and among-lakes scales. Our results indicated that there was a significant difference in macroinvertebrate assemblages among lakes under different trophic status, and total phosphorus was the chief environmental factor that regulated both taxonomic and functional beta diversity of macroinvertebrate assemblages. The abundances of pollution-tolerant species (e.g. *Limnodrilus hoffmeisteri* and *Microchironomus tabarui*) contributed the most to among-lakes dissimilarity. Functional beta diversity was significantly positively related with taxonomic beta diversity, but functional beta diversity was on average lower than taxonomic beta diversity. A combination of univariate- and multivariate techniques revealed that nutrient enrichment homogenized taxonomic and functional diversity of benthic macroinvertebrate assemblages in shallow lakes at within-lake and among-lakes scales, and that there was an overall trend towards taxonomic homogenization that exceeded the trend of functional homogenization. Thus, taxonomic and functional compositions should be considered simultaneously to improve understanding of the response of aquatic communities to anthropogenic disturbance, as the loss and gain of species may be influenced by species-specific features and functional composition may exhibit a relatively high correspondence with changes in environmental conditions.

Key words: eutrophication, beta diversity, functional homogenization, taxonomic homogenization, Chinese shallow lakes

Oral Session S04

STUDY ON TAXONOMY OF CHIRONOMINAE IN ZHEJIANG PROVINCE (DIPTERA, CHIRONOMIDAE)

Q.Q. Kong[1], Y.L. Li[1], X.L. Lin[2], X.H. Wang[2], X. Qi[1]
[1] College of Life Science, Taizhou University, Zhejiang, Taizhou 318000, China)
[2] College of Life Science, Nankai University, Tianjin 300071, China

In this study, 127 species of 32 genera of Chironominae are described and discussed in detail. Among the taxa, 1 tribe are newly recorded to Zhejiang; 4 genera are newly recorded to China; 13 genera are newly recorded to Zhejiang; 19 species are described as new to science; 10 species are newly recorded to China. Keys to species, genera in Zhejiang are given. The available data on geographical distribution are also reported.

1 tribe is newly recorded to China: Pseudochironomini.

19 species of 9 genera are described as new to science (including 17 species published in 2011–2017): *Dicrotendipes nudus* Qi, Lin & Wang, 2012, *Dicrotendipes saetanumerosus* Qi, Lin & Wang, 2012, *Dicrotendipes weiqiangensis* Qi, 2016, *Endotribelos redimiculum* Qi, Shi, Lin & Wang, 2013, *Manoa xianjuensis* Qi & Lin, 2017, *Microtendipes brevissimus* Qi, Shi, Lin & Wang, 2014, *Microtendipes globosus* Qi, Li, Wang & Shao, 2014, *Microtendipes zhejiangensis* Qi, Lin & Wang, 2012, *Nilothauma aristatum* Qi, Tang & Wang, 2016, *Nilothauma pandus* Qi, Lin, Wang & Shao, 2014, *Polypedilum* (*Polypedilum*) *constrictum* Zhang & Wang, 2017, *Polypedilum* (*Polypedilum*) *xianjuensis* Qi, 2016, *Polypedilum* (*Tripodura*) *cypellum* Qi, Shi, Zhang & Wang, 2014, *Polypedilum* (*Uresipedilum*) *minimum* Lin, Qi, Zhang & Wang, 2013, *Stenochironomus brevissimus* Qi, 2015, *Stenochironomus linanensis* Qi, 2015, *Stenochironomus xianjuensis* Zhang & Qi, 2016 and 2 unpublished species new to science: *Conochironomus obuncus* sp. n., *Dicrotendipes sinicus* sp. n..

4 genera are newly recorded to China: *Axarus* Roback, 1980, *Conochironomus* Freeman, 1961, *Endotribelos* Grodhaus, 1987 and *Manoa* Fittkau, 1963.

13 genera are newly recorded to Zhejiang Province: *Axarus* Roback, 1980, *Conochironomus* Freeman, 1961, *Endochironomus* Kieffer, 1818, *Endotribelos* Grodhaus, 1987, *Glyptotendipes* Kieffer, 1913, *Kiefferulus* Goetghebuer, 1922, *Parachironomus* Lenz, 1921, *Paracladopelma* Harnisch, 1923, *Xiaomyia* Sæther & Wang, 1993, *Cladotanytarsus* Kieffer, 1921, *Manoa* Fittkau, 1963, *Neozavrelia* Goetghebuer, 1941 and *Rheotanytarsus* Thienemann & Bause, 1913.

11 species are recorded for the first time to China: *Axarus fungorum* (Albu, 1980), *Cryptotendipes calyxus* (Guha, Das, Chaudhuri & Choudhuri, 1985), *Demicryptochironomus* (*Demicryptochironomus*) *ginzancedeus* Sasa & Suzuki, 2001, *Dicrotendipes inouei* Hashimoto, 1984, *Harnischia tenuitubercula* Chaudhuri & Chattopadhyay, 1990, *Kiefferulus umbtaticola* Yamamoto, 1979, *Paracladopelma hibarasecundum* Sasa, 1993, *Paratendipes subaequalis* (Malloch, 1915), *Polypedilum* (*Pentapedilum*) *tigrinum* (Hashimoto, 1983), *Polypedilum* (*Tripodura*) *harteni* Andersen & Mendes, 2010 and *Polypedilum* (*Uresipedilum*) *bingoparadoxum* Kawai, Inoue & Imabayashi, 1998.

Key words: Chironominae, Zhejiang, checklist, zoogeography, taxonomy

ASSEMBLING A COMPREHENSIVE DNA BARCODE REFERENCE LIBRARY FOR CHINESE NON-BITING MIDGES (DIPTERA: CHIRONOMIDAE)

X.L. Lin, X.H. Wang
College of Life and Sciences, Nankai University, Tianjin, China

At present, over 6000 species of non-biting midges (Diptera: Chironomidae) have been recorded worldwide including Antarctic, estimating from 20000 to 40000 species, and about 1000 of which have been found in China. Chironomids are promising bioindicators for aquatic monitoring due to their high diversity and adaption to different habitats. However, their utility for biomonitoring was historically limited by difficulties in their morphological identification, particularly in the immature stages. DNA barcoding using a fragment of the mitochondrial cytochrome *c* oxidase subunit 1 gene (COI) has proven to be successful for species-level identification in chironomids. Our goal is to assemble a comprehensive DNA barcode reference library of chironomids as a reference resource for research and management of biodiversity in China. Currently, more than 350 Chinese chironomid species including 1400 COI barcodes have been registered in the public, open-access database (BOLD), along with their individual images, geo-references and other relevant laboratory data. Our preliminary results indicate that the majority of morphospecies could be differentiated by DNA barcodes with an average threshold at 4–5% which is larger than other insect groups. In addition, the immature stages are associated with adults by DNA barcodes successfully. Moreover, a number of cryptic species have been detected by DNA barcodes, and then confirmed by additional nuclear genetic markers and morphological observations. A comprehensive DNA barcode reference library of chironomids in China is under development and will be widely used for scientific research, education and aquatic conservation.

Key words: COI, cryptic species, misidentification, genetic distance, China

THE LARVAE OF *EPEORUS DAYONGENESIS* AND *E. HERKLOTSI* FROM CHINA (EPHEMEROPTERA: HEPTAGENIIDAE)

Z.X. Ma, W. Zhang, N. Han, C.F. Zhou
College of Life Sciences, Nanjing Normal University, 210023, Nanjing, P. R. China

There are 17 described *Epeorus* species in China but 10 of them are known from adults only. In recent years, some immature stages of those species are collected and associated with image stage. Here the larvae of two species *E. herklotsi* (Hsu, 1936) and *E. dayongensis* (Gui and Zhang, 1992) are described and photographed. The nymphs of *E. herklotsi* have two big submedian spines on posterior margin of abdominal terga 1-9, dense hairs on anterior margin of head capsule and sucker-like gill lamellae. The nymphs of *E. dayongensis* is characterized by the following features: abdominal terga 1-10 bear line of acute posterior marginal spines, terga 2-9 have a pair of big acute submedian spines, gills with sclerotized line situated a distance from anal margin, middle and hind legs with patella-tibial suture.

Key words: *Epeorus*, China, nymph, Heptageniidae, Ephemeroptera

OVERVIEW OF PHILIPPINE STONEFLIES (INSECTA: PLECOPTERA) WITH NEW RECORDS OF *NEOPERLA* NEEDHAM, 1905 FROM MINDORO ISLAND

A.L. Pelingen, H. Freitag
Department of Biology, School of Science and Engineering, Ateneo de Manila University, Loyola Heights, Quezon City 1101, Philippines

Taxonomic research dealing with Plecoptera (stoneflies) is one of the most overlooked gaps in freshwater studies in the Philippines, despite stoneflies' high suitability as bioindicators of clean freshwater systems. In the tropics, stoneflies have low diversity on family level though, due to the geologic profile of the country, species richness and endemism are expected to be high. Presently, Philippine representatives comprise three stonefly families: Perlidae, Peltoperlidae, and Leuctridae, with four genera, namely *Neoperla* Needham, 1905 (Perlidae); *Phanoperla* Banks, 1938 (Perlidae); *Peltoperla* Needham, 1905 (Peltoperlidae); and *Rhopalopsole* Klapálek, 1912 (Leuctridae). From these genera, 41 species were documented in a few limited studies within a century, however, all of them from Greater Luzon and Mindanao. We provide a checklist of the Philippine stoneflies with new records from Mindoro. Large knowledge gaps in stonefly diversity and distributions are pointed out and specific taxa are discussed briefly.

Key words: Plecoptera, *Neoperla*, Philippines

TAXONOMY AND DISTRIBUTION OF AQUATIC OLIGOCHAETES (ANNELIDA: OLIGOCHAETA) IN TIBET, CHINA

Y. Peng[1,2], Y.D. Cui[1]
[1] State Key Laboratory of Freshwater Ecology and Biotechnology, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan 430072, China
[2] University of Chinese Academy of Sciences, Beijing 100049, China

The Qinghai-Tibetan Plateau is one of global biodiversity hotspots and considered to be unique in its biota. However, there have been limited studies on aquatic oligochaetes (Annelida: Oligochaeta) of the Qinghai-Tibetan Plateau. The present paper embodies the results of a comprehensive investigation of aquatic oligochaetes from South Tibet, Southeast Tibet, North Tibet and Central Tibet in 2013~2016. The research includes classical taxonomy, fauna analysis and distribution pattern.

In terms of taxonomy, a systematic account of 47 species belonging to 3 families and 22 genera of aquatic oligochaetes is presented (see the list), doubling the total number of known species. Among them, 6 species of 3 genera are described as new to science; 2 species of 2 genera are regarded as new recorded species in China; 8 species of 8 genera are regarded as new recorded species in Tibet. Some species of *Tubifex* and *Isochaetides* are re-described.

Cluster analysis reveals that the fauna of aquatic oligochaetes in Tibet is close to areas such as North America and Europe, and less similar to areas such as Central Asia, India and Japan, thus being more Holarctic. Dealing with Tibet itself, the fauna in Central Tibet is close to Southeast Tibet, and that in South Tibet is similar to North Tibet. The species of Tubificinae are rich in Tibet, in particular, *Tubifex*, and the known species of this genus in China have increased from 1 to 7. There are 9 species reported only from Tibet.

Based on data of aquatic oligochaetes in lakes of the Qinghai-Tibetan Plateau, Yunnan-Guizhou Plateau, Neimenggu-Xinjiang Plateau and Eastern Plain of China, the distribution pattern of aquatic oligochaetes along elevation is analyzed. The results indicate that the species number of aquatic oligochaetes shows a decreasing trend with the increase of elevation. The elevational tolerance range of species does not increase with the increase of elevational optimum of species, which does not support Rapoport's elevational rule: species at higher elevations have greater elevational ranges. The standing crop and body size of aquatic oligochaetes do not show obvious trends along elevation, but both exhibit larger variation ranges in low elevation than in high elevation. The mechanism analysis reveals that the decline of species diversity of aquatic oligochaetes with the increase of elevation is mainly due to decreasing water temperature and increasing salinity; water surplus and deficit (mean annual precipitation minus mean annual evaporation) increases with the rise of elevation, and thus raising water salinity.

Key words: Tibet, Oligochaeta, morphology, fauna, macroecology, elevation, distribution pattern

ANALYSIS OF TAXONOMY OF FAR EASTERN UNIONINAE AND ANODONTINAE (UNIONIDAE, BIVALVIA)

E.M. Sayenko[1], M. Soroka[2]
[1] Federal Scientific Center of the East Asia Terrestrial Biodiversity, Far Eastern Branch of Russian Academy of Sciences (FSCEATB FEB RAS), 159 Stoletiya Street, Vladivostok 690022, Russia
[2] Department of Genetics, University of Szczecin, Szczecin 71-412, Poland

Till now many questions of bivalves' classification remain unresolved. Among freshwater bivalves, taxonomy of family Unionidae Rafinesque, 1820 causes the greatest number of questions. On the basis of our own and literary data, including conchological characters of shells of adult mollusks, larvae (glochidia) and the results of genetic investigations, a critical analysis of the taxonomy of Far Eastern Unionidae, namely, the subfamilies Unioninae and Anodontinae, is carried out. The systematic position of some unionid taxa from Asia and Russian Far East is given, with a few changes and corrections; the problems of the species taxonomy are not rise.

Since last century numerous revisions were accumulated using various methods: first, the system was mainly used conchological features (shell shape, umbonal sculpture, etc.) and, less commonly, differences in anatomy of adult mollusks; then, morphological characters of larvae (glochidia) shells; finally, genetic data (primarily DNA sequences of the mitochondrial genes and their genetic variation characteristic for intra- and interspecific level).

Our preliminary investigation did not confirm a synonymy of the genus *Middendorffinaia* (Russian Far East) with genera *Nodularia*, *Inversiunio* or species *Inversidens pantoensis*; from the other hand, we found *Middendorffinaia* is close to Japanese species *Nodularia (=Unio) biwae*. Genus *Sinanodonta* is distinguished from Far Eastern *Anemina* and European *Anodonta*. Taxonomy position of the anodontins *Anemina*, *Buldowskia* and *Amuranodonta* are still under discussion, so does relations between the taxa *Beringiana* and *Kunashiria*.

Key words: Bivalvia, Unionidae, Unioninae, Anodontinae, glochidia, molecular phylogenetics

AN EVOLUTIONARY ECOLOGICAL STUDY OF THE GIANT WATER BUG *APPASUS JAPONICUS*: DETECTION OF THEM EXHIBITING ASYMMETRIC REPRODUCTIVE ISOLATION

T. Suzuki[1], K. Tojo[1,2]
[1] Department of Biology, Faculty of Science, Shinshu University, Asahi 3-1-1, Matsumoto, Nagano 390-8621, Japan
[2] Institute of Mountain Science, Shinshu University, Asahi 3-1-1, Matsumoto, Nagano 390-8621, Japan

Identification of factors leading to speciation and elucidation of the mechanisms thereof with respect to biodiversity creation are considered to be important tasks to be addressed by many biologists. Especially with regard to the process of evolution and speciation among closely related species living on continent and surround islands, there is much research being conducted in order to elucidate the history of such speciation based in molecular phylogenetic analysis. In this study, we focus on the giant water bug, *Appasus japonicus*, which is distributed in the Japanese Archipelago, the Korean Peninsula and Northeastern China. Our previous study revealed that there is a difference in the shape of their parameres between the Korean and the Japanese populations (Korean populations: 'wave-like', Japanese populations: 'hook-like'). In addition, the Korean *A. japonicus* and the sister species, *Appasus major*, have very similar 'wave-like' shaped parameres. Because of the 'wave-like' shaped parameres being shared between different species of the same genus, it is considered that the 'wave-like' shape is an ancestral characteristic. On the other hand, from the results of our previous molecular phylogenetic analyses of their mtDNA, it was shown that the Japanese populations of *A. japonicus* are the ancestral lineage, and that 'back dispersal' from the Japanese Archipelago to the continent occurred. Therefore, there is an apparent discrepancy between the results as interpreted based on the shape of parameres and those based on the molecular phylogenetic analysis of mtDNA as to which of the Korean or the Japanese populations are in fact ancestral. In addition, our previous study also revealed that *A. japonicus* had clearly genetically differentiated into three clades (Korean, Southwestern Japanese and Northeastern Japanese populations). Therefore, in this study, we performed mating experiments, that were using individuals from each of the three different clades as determined by their mtDNA, and microsatellite analysis to estimate the population structure of their nDNA. As a result, it was revealed that although Korean males can copulate with Japanese females, Japanese males can not copulate with Korean females. Furthermore, as a result of the microsatellite analysis, it was shown that there is a high possibility that mating between different linages occurs in the Japanese Archipelago. Based on the above results, the shape of parameres of the Japanese population evolved into a 'hook-like' shape subsequent to genetic differentiation between the Korean and Japanese populations occurring, and it is thus considered to be in the incipient stage of speciation.

Key words: Belostomatidae, premating isolation, speciation, phylogeography, SSR

EXTREMELY LARGE GENETIC DIFFERENTIATION IN THE MAYFLY *DIPTEROMIMUS TIPULIFORMIS*: AN IDEAL CASE IN ELUCIDATION OF THE MECHANISMS OF SPECIATION (EPHEMEROPTERA; DIPTEROMIMIDAE)

M. Takenaka, K. Tojo
Department of Biology, Faculty of Science, Shinshu University, Asahi 3-1-1, Matsumoto, Nagano 390-8621, Japan

Speciation is lead by the evolution and maintenance of reproductive barriers between populations. Thus, the establishment of an isolation barrier is an essential step and primary factor in promoting speciation. *Dipteromimus tipuliformis* is adapted to the narrow headwater regions of river systems, each population being fragmented and generally relatively small in size. That is, their populations tend toward miniaturization, and they are usually scattered and isolated, having a patchy distribution. As a result, their potential for gene flow between populations is extremely limited, and so there is a higher potential for genetic differentiation between populations, and the influence of random genetic drift is also high. Hence, we particularly note that the degree of their genetic differentiation between populations relative to their geographical distance is large. In the present study, we analyzed the DNA sequences of their mitochondria DNA COI and 16S rRNA, and the nuclear DNA histone H3 and 28S rRNA regions. As a result of these analyses, we revealed that the scale of genetic differentiation observed within *Dipteromimus tipuliformis* species is comparable to a level of genetic differentiation typical at the interspecific level or greater, when comparing them with other related mayfly groups. Due to the observation of such large genetic differentiation, we established a successful artificial mating technique, *i.e.*, a "hand-pairing" based breeding method for mayflies. Furthermore, we also succeeded in clearly verifying by a genotyping method that the offspring reproduced by the "hand-pairing" were in fact derived from the actual male and female which were used for "hand-pairing". We report here, the developmental and hatching rates of egg batches from females, which were copulated by hand-pairing methods between each clade and/or different clades. As results, we revealed that *Dipteromimus tipuliformis* have been exhibited speciation continuum, called as the "ring species". Thus, our research targeting this mayfly encompasses a significantly important meaning in investigating of the speciation mechanism.

Key words: Japanese endemic family, Phylogeography, reproductive experiment, hand-pairing, speciation

TAXONOMY OF THE FAMILY BAETIDAE (INSECTA: EPHEMEROPTERA) IN CHINA

X.L. Tong, W.F. Shi
Department of Entomology, College of Agriculture, South China Agricultural University, P.R. China

The Baetidae is the largest family of Ephemeroptera and almost 100 genera and 1000 species have been described in the world. Baetid larvae widely distributed in various freshwater habitats and are most commonly encountered the component of benthic macroinvertebrates during the study of freshwater ecology or bio-assessment. In view of their important role in water quality monitoring and health assessment of freshwater ecosystem, the demands for the knowledge of taxonomy of baetid larvae are growing constantly in China. China is across the Palaearctic and Oriental regions and should possess an enormous diversity of baetids, yet its taxonomy remains poorly understood. In this study, 14 genera and 105 species of Baetidae, including 48 new species and 25 newly recorded species, are recognized from China based on examination of more than 20000 baetid specimens deposited in the authors' collection (SCAU) collected from the majority of parts of the country since 1995.

Key words: Mayfly, Baetidae, species diversity

PHYLOGENY OF THE SUBFAMILY MACRONEMATINAE (TRICHOPTERA: HYDROPSYCHIDAE) BASED ON MOLECULAR AND MORPHOLOGICAL ANALYSES

J.C. Uy Christine[1], J.H. Kang[2], Y.J. Bae[1,2,3]
[1] Department of Life Sciences, Graduate School, Korea University, Seoul, South Korea
[2] Korean Entomological Institute, Korea University, Seoul, South Korea
[3] Division of Environmental Science and Ecological Engineering, College of Life Sciences and Biotechnology, Korea University, Seoul, South Korea

The phylogenetic relationships within the members of Trichoptera subfamily Macronematinae Ulmer have long been revised and debated. Our study, based on mitochondrial cythochrome oxidase I (*COI*; 658 bp) and nuclear D2 gene sequences (687 bp), found all genera to be monophyletic except for the genera *Macrostemum* Kolenati and *Polymorphanisus* Walker. *Leptonema* Guerin-Meneville was found to be the basal clade in the subfamily. Two previously known tribes (Macronematini and Polymorphanisini) were not supported. We also found that the genera *Centromacronema* Ulmer, *Baliomorpha* Neboiss, and *Macronema* Pictet are most closely related having three head setal wart counts, and unsegmented inferior appendage of male genitalia, as their synapomorphy. We confirmed that genera *Amphipsyche* McLachlan and *Protomacronema* Ulmer are the most closely related. Ancestral state reconstruction (ASR) of five chosen diagnostic morphological characters in the subfamily Macronematinae showed that possession of mouthparts, forewing discoidal cell, forewing crossvein sc-c, two-segmented inferior appendage of male genitalia and numerous head setal warts are ancestral states. The head setal wart, which is unique organ in Trichoptera, evolved towards a decreasing number in the whole subfamily. This first molecular phylogenetic study, covering 16 out of 17 genera in the subfamily Macronematinae and including the ancestral reconstruction of five key characters, provides an important basis to understand long-standing questions regarding its phylogenetic relationships.

Key words: Trichoptera, Macronematinae, phylogeny, COI, ancestral stat reconstruction

GENETIC DIVERSITY OF *CLOEON* SPECIES IN EAST ASIA: WITH SPECIFICAL REFERENCE TO THE SPECIFIC LINEAGE OF *CLOEON DIPTERUM*

K. Yano, K. Tojo
Department of Biology, Faculty of Science, Shinshu University, Nagano, Japan

The *Cloeon* mayflies are widely distributed throughout the world. Perhaps their special ecological characteristics, such as the presence of parthenogenetic lineage(s), ovoviviparous reproduction, may contribute to their widespread distribution. Thus, some *Cloeon* species are known for their ovoviviparous reproduction, despite almost all other insects being known as "oviparity". In the oviparous insects, females develop eggs (oocytes) that accumulate all of the nutrients required during embryonic development (e.g., yolk proteins, lipids). However, as a unique reproductive strategy, "ovoviviparous" reproduction is also sometimes observed. Furthermore, "viviparity" is also known to exist in a very few insects. Embryogenesis of viviparous insects progresses by nutrition supplied from the mother. Under such circumstances, we obtained intriguing data suggesting viviparous reproduction in *C. dipterum* in the East Asian region. So far, we have conducted a molecular phylogenetic analysis of *Cloeon* mayflies and have clarified the existence of a unique genetic lineage in the East Asian region. For *C. dipterum*, a recent study revealed 6 genetically differentiated haplotype groups; the group "CT1" is distributed in Europe and Canada, "CT2-3" in Europe, and "IS1-3" is distributed mainly in the Macaronesian Islands. We conducted a genetic analysis of the sequence data of many *C. dipterum* specimens collected from across the Japanese Islands and the Korean Peninsula. Then, by integrating with *C. dipterum* sequence data from around the world, we attempted a phylogenetic discussion. As a result of our phylogenetic analysis, the existence of a new East Asian genetic lineage was observed. The viviparous reproduction as mentioned above was also suggested in this lineage. In our observations of the Japanese specimens, embryogenesis progressed within the mother's body, and nymphs also hatched within the mother's body. Moreover, from our histochemical observations during their embryogenesis, no eosinophilic proteinous yolk granules were observed. On the other hand, lipids were observed in the eggs, and these lipids decreased with the progress of embryogenesis. Yolk proteins are essential nutrients in the developments of embryos. If proteinous yolk granules are lacking in the eggs, it is then necessary that protein is supplied directly from the maternal host. Thus, at least for the Japanese lineage, we suggest that they are not ovoviviparous mayfly, but rather a viviparous mayfly. In addition, we compared them with the reproduction styles of other "viviparous" insects. As a result of that comparison, it was suggested that the viviparity of *C. dipterum* in Japan may be a unique new variant system.

Key words: mayfly, embryology, phylogeny, the Japanese archipelago, genetic structure

A REVISED REVIEW ON *CINYGMINA* OF CHINA (EPHEMEROPTERA: HEPTAGENIIDAE: ECDYONURINAE)

W. Zhang, Z.X. Ma, N. Han, C.F. Zhou
College of Life Sciences, Nanjing Normal University, 210023, Nanjing, P. R. China

The species in the genus *Cinygmina* have frequently reported and mentioned in the literatures. The adults of them are easily identified but their nymphal stages are very difficult to separate. In this study, we checked all types and associated materials in our collection to look for solid characters to differentiate both imaginal and nymphal stages. As a result, we find that the color patterns on head and body of them are stable and different between species. So this character is adopted to classify species of this genus. The known four species can be divided into two groups. The *Cinygmina obliquistrita* and *C. rubromaculata* have two rows of pale dots on head near anterior margin of nymph while the counterparts of *C. yixingensis* and *C. hunanensis* have no distinct dots. The former two species can be differed further by the color pattern of abdominal terga: the *C. obliquistrita* has additional typical oblique stripes but the *C. rubromaculata* has no this kind of stripes. Furthermore, the latter two species, which have no obvious pale dots on head, can be separated by the abdominal color patter too although both of them have pale terga 5, 8 and 9: each tergum of *C. yixingensis* has a pair of pale dots but those dots extended into short stripe or belt in *C. hunanensis*. The nymph of *C. furcata* is kept unknown. The adults of them are easily differentiated by their genitalia and abdominal color.

Compared to other genera of the subfamily Ecdyonurinae, the genus *Cinygmina* have both mature and immature autapomorphies. So it is treated as a valid genus not the junior synonym of the *Afronurus*.

Key words: Heptageniidae, *Cinygmina*, morphology, taxonomy, phylogeny

MOLECULAR IDENTIFICATION OF THE INTERMEDIATE OF TWO PROXIMAL SPECIES OF *LIMNODRILUS* (OLIGOCHAETA, NAIDIDAE) BASED ON 16S rDNA AND COI SEQUENCES

T.T. Zhou[1,2], Y. Peng[1,2], Y.D. Cui[1]
[1] State Key Laboratory of Freshwater Ecology and Biotechnology, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan 430072, China
[2] University of Chinese Academy of Sciences, Beijing 100049, China

Limnodrilus hoffmeisteri and *L. claparedeianus* are common species of the *Limnodrilus*. They are distinguished from each other by the ratio of the length to width of the penial sheath and the values of them are 8-14 and 20-80, respectively. However, there are some intermediates which are hard to differentiate in identification process. *L. hoffmeisteri* and similar species which were taken from Yangtze River basin (East Lake and Longgan Lake) and Huaihe River basin have been differentiated by using morphology and molecular biology technology in this study. All the sequences were spliced, calibrated and blasted. We found that the similarity rate between the intermediates and *L. claparedeianus-cervix* reached 98%-100%. The calculations of the uncorrected pairwise genetic distances depended on MEGA. The mean distances between species were much more than 10 times higher than the mean divergences within them which proved that the feasibility of molecular technology in classification and identification. The 16S rDNA gene tree showed general agreement with the COI tree. The conclusion shows that: *L. hoffmeisteri* is a complex species; *L. claparedeianus-cervix* forms a separate branch which is closer to *L. hoffmeisteri* than *L. claparedeianus*. Combining with the length/width ratio of the penial sheath of *L. claparedeianus-cervix*(15-27), we consider that it is a cryptic species of *L. hoffmeisteri*.

Key words: 16S rDNA, COI, *Limnodrilus*, morphology

LAND USE CHANGES AND SOCIO-ECONOMIC DEVELOPMENT DETERIORATING RIVER ECOSYSTEM HEALTH IN HAIHE RIVER BASINS, CHINA

X. Cheng[1], R.H. Sun[1], D.Y. Wu[2]
[1] State Key Laboratory of Urban Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, No. 18 Shuangqing Road, Haidian District Beijing, 100085 China
[2] Hengshui University, No. 1088 West Heping Road, Hengshui Hebei, 053000, China

It is important to assess river ecosystem health in large-scale basins when considering the complex influence of anthropogenic activities on these ecosystems. This study investigated the river ecosystem health in the Haihe River Basin (HRB) by sampling 148 river sites during the pre- and post-rainy seasons in 2013. An assessment model was established to assess the river ecosystem health based on water physicochemical, nutrients, and macroinvertebrate indices, and the health level was divided into "very poor," "poor," "fair," "good," and "excellent" according to the health score calculated from the model. The assessment results demonstrated that (1) the overall status of river ecosystem health of the HRB was "poor"; (2) no catchments showed "excellent"and the percentages of catchments of the rest four river ecosystem health catogories were 12.88%, 40.91%, 40.15%, and 6.06%, respectively; (3) the macroinvertebrate health levels were improved from "poor" to "fair" after the rainy season. The results of a redundancy analysis (RDA), path analysis of the structural equation model (SEM), and X-Y plots indicated that the land use types of forest land and grassland had positive relationships with river ecosystem health, whereas arable land, urban land, gross domestic product (GDP) per capita, and population density had negative relationships with river ecosystem health. The variance partitioning (VP) results showed that anthropogenic activities (including land use and socio-economy) together explained 30.9% of the variations in river ecosystem health in the pre-rainy season, and this value increased to 35.9% in the post-rainy season. Land use intensity was the first driver of river ecosystem health, and land use variables explained 20.5% and 25.7% of the variations in river ecosystem health in the pre- and post-rainy season samples, respectively. Socio-economic activities was the second driver and socio-economic variables explained 12.3% and 17.2% of the variations, respectively. The SEM results revealed that urban land had the strongest impact on water quality health and that forest land had the strongest impact on macroinvertebrate health. This study has implications for the selection of appropriate indicators to assess river ecosystem health and generated data to examine the effects of anthropogenic activities on river ecosystem health in a rapidly growing region.

Key words: Haihe River Basin, river ecosystem health, land use, socio-economic development, macroinvertebrates

COMMUNITY AND POPULATION DYNAMICS OF BENTHIC MACROINVERTEBRATES IN RESPONDING TO DISTURBANCES IN STREAMS

T.S. Chon[1,2], G. Kwak[1], Y.H. Jang[1], N. Jung[3], J.B. Leem[1]
[1] Ecology and Future Research Association, Busan (Pusan) 46228 Republic of Korea
[2] Division of Biological Sciences (Prof. Emer.), Pusan National University, Busan 46241 Republic of Korea
[3] Department of Physics, Inha University, Incheon 22212 Republic of Korea

Benthic macroinvertebrate communities were surveyed in streams across different levels of natural (e.g., flooding) and anthropogenic (e.g., pollution) disturbances in the southern peninsula of Korea. At the sites with least pollution, species abundance distributions (SADs) were remarkably stable consisting of three groups, a small number of the most dominant species, a large number of intermediately abundant species, and rare species. With a slight level of disturbance the community structure responded adaptively along with the energy subsidy effect. In responding to a strong level of anthropogenic disturbance SADs were differentiated from log-normal pattern to geometric pattern, causing a fundamental change in community structure. In responding to natural disturbances (e.g., flooding), in contrast, a partial differentiation was observed to cause decrease in the levels of intermediately abundant species, without changing the SAD pattern too much. When biotic potential (i.e., fecundity) and external environment (e.g., pollution) matched, populations (e.g., chironomids) in streams abnormally erupted. Beta diversity accordingly reflected changes in community structure in responding to environmental impacts in spatial domain in river networks. Prediction and management of stream communities were additionally discussed in the presentation regarding achievement of sustainability in aquatic ecosystems.

Key words: community structure, ecological integrity, aquatic ecosystems, environmental impact, population dynamics

STUDY ON THE DAILY DRIFT BEHAVIOR OF MACROINVERTEBRATE IN THE XIANGXI RIVER

Y. Du[1,2], Y.H. Zhang[1,2], X. Zhu[1,3], M. Zhang[1], G.F. Yang[2], X.D. Qu[1]
[1] Water Environment Institute, China Institute of Water Resources and Hydropower Research, Beijing, P.R. China
[2] College of Water Conservancy, Shenyang Agricultural University, Shenyang, P.R. China
[3] Qufu Normal University, College of geography and tourism, Rizhao, P.R. China

Drift behavior is an important biological adaption of macroinvertebrates in the lotic ecosystems driven by the hydrological process. And the drift behavior play a key role in the studies of spatial and temporal distribution of macroinvertebrates in streams, it is of great significance for re-understanding the formation process and evolution mechanism of the vertical pattern of river ecosystems. In order to identify the community structure of drifted macroinvertebrates, reveal the drift behavior rhythms, and compare its functional feeding groups, the drifted macroinvertebrates were sampled and studied from two tributaries of Xiangxi River (Jiuchong Stream and Gaolan Stream) in August, 2017. The results shows that Ephemeroptera is the dominant taxa with relative abundance of 76.9% and 96.1% in the Jiuchong Stream and Gaolan Stream, respectively. The taxa richness of the drifted macroinvertebrates was much higher in the Jiuchong Stream (35 species) than the Gaolan Stream (14 species). The dominant species taxa are *Epeorus* sp., *Drunella* sp., *Baetis* sp., *Baetiella* sp., *Ecdyonurus* sp., *Limnophilidae* sp., *Philopotamidae* sp. and *Simulium* sp. in the Jiuchong Stream. And the dominant taxa are *Baetiella* sp. and *Epeorus* sp. in the Gaolan Stream. The nocturnal drifting pattern was identified the highest density of drifted macroinvertebrates appeared at 06:00 am in those two streams. The primary nocturnal drifter was taxa of Plecoptera in the Jiuchong Stream and taxa of Ephemeroptera in the Gaolan Stream. In comparing with drift behavior of different taxa, the drift patterns are more species-specific. Five taxa showed similar drift behavior and the highest density appeared between 20:00 and 22:00, including *Epeorus* sp., *Drunella* sp., *Ecdyonurus* sp.,Limnophilidae sp., Philopotamidae sp. and *Simulium* sp. The highest density of *Baetis* sp. appeared between 04:00 and 06:00. The highest density of *Baetiella* sp. appeared between 04:00 and 06:00 in the Jiuchong Stream, and between 02:00 and 04:00 in the Gaolan Stream. The composition of functional feeding groups and life-form variated between the day time and night time. However, collector-gatherers and swimmers dominated the functional feeding groups and life-forms. Our studies shown that human disturbance play an important role in structuring the drifting behaviors and rhythms between the Jiuchong Stream and Gaolan Stream.

Key words: Xiangxi River, macroinvertebrate, drift behavior, drift rhythm, drifting density

A HISTORICAL REVIEW ON MOSQUITO CONTROL RESEARCH IN VIETNAM

V.C. Duong[1], W.G. Kim[1], N. Sareein[1], J.S. Kim[1], V.V. Nguyen[2], Y.J. Bae[1]
[1] Department of Environmental Science and Ecological Engineering, Korea University, Seoul, Korea
[2] Faculty of Biology, VNU University of Science, 334 Nguyen Trai, Thanh Xuan, Hanoi, Vietnam

The first comprehensive study on the family Culicidae that contributed for the understanding of the mosquito's diversity from Vietnam was in 1930 by Borel, who reported 24 species from the Southern Vietnam. According to the current data available on the Systematic Catalog of Culicidae website, 227 mosquito species are recorded in Vietnam, which represents the 22.5% of the reported for Southeast Asia (1,001 species). Based on the literature, most of the taxonomic studies are primarily morphologic, while molecular and genetic data are still uncovered. The mosquitoes in Vietnam are also recognized as crucial vectors of many vertebrate pathogens such as Malaria, Dengue fever, Chikungunya, Yellow fever, Lymphatic filariasis, Japanese encephalitis and Zika virus. Thus, several strategies have emerged to eliminate and prevent the mosquito-borne diseases. For example, chemical control such as DDT or Pyrethroid that have been used extensively in Vietnam caused vector resistance, harmful effects in human health and to the environment. On the other hand, in small-scale, biological control agents such as Bativec larvicide (*Bacillus thuringiensis*), copepods of the genus *Mesocyclops* or larvivorous fish have been used and resulted successful in controlling mosquitoes with little adverse effects. In spite of the aquatic predaceous insects have been proved to be low cost-effective in reducing human-vector contact, this concept is still uncommon in the country. Therefore, suitable rearing and controlled methods to produce a mass production of predaceous insects are being studied in order to evaluate these organisms as potential biological control agents.

Key words: Diptera, Culicidae, mosquitoes, taxonomy, vector control strategies, Vietnam

METACOMMUNITY STRUCTURE AND ASSEMBLY MECHANISM OF MACROINVERTEBRATE AND DIATOM WITHIN THREE INTERMEDIATE STREAM NETWORKS LOCATED AT DIFFERENT GEOGRAPHIES

S.W. He, K. Chen, A.R. Rajper, N. Ding, B.X. Wang
Department of Entomology, Nanjing Agricultural University, Nanjing 210095 P.R. China

Currently, the metacommunity framework including two main features i.e. metacommunity structure and mechanistic become a popularity framework to understanding the species distributions and community assembly rules. However, studies simultaneously assessing species distribution and assembly mechanism on multiple metacommunities are rare. The combination of two metacommunity features may provide a comprehensive understanding of biogeographical arrangements that is a major concern in ecology. Here we aimed to reveal geographical pattern of the species distributions and then examine the assembly rules of stream metacommunities of 3 intermediate basins across low to high latitudes in China, and performed separate analyses on different spatial hierarchies (i.e. whole stream network scale vs. headwaters and mainstreams). We applied the same set of macroinvertebrate and diatom data to test structure via the elements of the metacommunity structure analysis, and compare the importance of environmental and dispersal-related processes via distance-decay relationships (DDRs) analysis. Our community datasets were best fitted with a compartmentalized Clementsian or quasi-Clementsian structure among three basins, indicating that it was a weak geographical effect on variation in stream metacommunities structure. This geographical structure pattern likely scale-dependent and seems related to the geographical variability in environmental gradients within basin. In our study, all of community similarities were significant related to environmental distances, suggesting that environmental filtering prevails in three intermediate basins. More importantly, we found the level of environmental control was strongest at highest environmental heterogeneity basin, highlighting that it was a strong geographical effect on variation in contribution of species sorting process. Results showed the influence of environmental filtering was strong in more isolated headwaters, whereas dispersal-related process was important in well-connected mainstreams, demonstrating that dendritic stream networks covered an intermediate extent also exhibit unique mechanistic dynamics. Moreover, we found macroinvertebrates showed stronger environmental control than diatoms, suggesting that macroinvertebrates are better able to track environmental variation than diatoms. Together, our results suggest the importance of multiple factors such as geography, spatial scale, organism and dendritic network characteristics should be considered when studying metacommunities structures and mechanisms dynamic in stream ecosystems.

Key words: geographies, environmental variation, metacommunity framework, species sorting, distance-decay, aquatic organisms

MULTIPLE FACETS OF STREAM MACROINVERTEBRATE ALPHA DIVERSITY ARE DRIVEN BY DIFFERENT ECOLOGICAL FACTORS ACROSS AN EXTENSIVE ALTITUDINAL GRADIENT

Z.F. Li[1], X.M. Jiang[1,2], J. Wang[1], X.L. Meng[1], J. Heino[3], Z.C. Xie[1]
[1] The Key Laboratory of Aquatic Biodiversity and Conservation, Institute of Hydrobiology, Chinese Academy of Sciences, Hubei 430072, China
[2] Biodiversity Centre, Finnish Environment Institute, Paavo Havaksen Tie 3, P.O. Box 413, 90014 Oulu, Finland
[3] University of Chinese Academy of Sciences, Beijing 100049, China

Aim: Environmental filtering and spatial structuring are important ecological processes for the generation and maintenance of biodiversity. However, the relative importance of these ecological drivers for multiple facets of diversity is still poorly understood in highland streams. Here, we examined the response of three facets of stream macroinvertebrate alpha diversity to local environmental, landscape-climate and spatial factors in a near-pristine highland riverine ecosystem on Earth.
Location: Southern Tibet, China.
Methods: Species richness (SRic), functional (FRic, FEve, FDiv and RaoQ) and phylogenetic alpha diversity (AvTD and VarTD) were calculated for 55 streams with a total of 195 macroinvertebrate species. Pearson correlation coefficient was used to detect spatial congruence among the diversity indices. Multiple linear regression models (MLR) and variation partitioning were used to identify the relative importance of different ecological drivers.
Results: FRic showed relatively high concordance with SRic, while AvTD and VarTD were quite independent from SRic but correlated positively with FEve and RaoQ. Species richness and functional diversity indices were more strongly determined by environmental variables, while phylogenetic diversity indices were better explained by spatial factors. In terms of environmental variables, habitat-scale variables related habitat complexity and water physical features played the primary role in determining the diversity patterns of all three facets, whereas the influence of landscape variables appeared less influential.
Main conclusions: Our findings showed that both environmental and spatial factors are important ecological drivers for biodiversity patterns of macroinvertebrate in Tibetan streams, although their relative importance was contingent on different facets of diversity. Such findings verified the complementary roles of taxonomic, functional and phylogenetic diversity, and highlighted the importance of comprehensively considering multiple ecological drivers for different facets of diversity in biodiversity assessment. Besides, we also argue that protecting diverse local habitat conditions may be an effective strategy for biodiversity conservation in highland freshwater ecosystems.

Key words: macroinvertebrate, species richness, functional diversity, phylogenetic diversity, ecological drivers, highland streams

COMMUNITY STRUCTURE OF MOLLUSCS AND THEIR RELATIONSHIP WITH ENVIRONMENTAL FACTORS IN SOUTH DONGTING LAKE

Z.Y. Liu[1,2]
[1] The Key Laboratory of Aquatic Biodiversity and Conservation, Institute of Hydrobiology, Chinese Academy of Sciences, Hubei 430072, China
[2] University of Chinese Academy of Sciences, Beijing 100049, China

From April 2013 to January 2015, six surveys of mollusc resources were carried out on 5 sections in the South Dongting Lake. A total of 29 species of molluscs, 2 classes, 9 families, 20 genera, were detected. Among them, there are 8 generas and 15 species of Gastropoda, 12 generas and 14 species of Bivalves, and 62% of them were endemic species of China. The species richness in each section were 24 species and 20 species in Wan Zi lake and Dongnan Lake respectively, and the number of entry species in the Zi River was the lowest, only 13 species. The average density of molluscs in southern Dongting Lake is 11.98 ind./m^2, with an average biomass of 26.70 g/m^2. The average density of Gastropods and Bivalves are 10.31 ind./m^2 and 1.66 ind./m^2, respectively, and the average biomass is 19.29 g/m^2 and 7.41 g/m^2, respectively. ANOSIM analysis showed that there was no significant difference in mollusc community structure between each section. SIMPER analysis showed that the top three dominant species in southern Dongting Lake were *Bellamya aeruginosa*, *Rivularia auriculata* and *Rivularia calcarata*. The average Shannon-Wiener, Simpson diversity and Pielou evenness index were 1.19, 1.21 and 0.54 respectively. Compared with the historical survey, the molluscs in south Dongting Lake showed a trend of increasing number of Gastropods and decreasing number of Bivalves. The ABC curve showed that the mollusc community structure in the South Dongting Lake was in a moderate disturbance state. Pearson correlation analysis showed that water depth, ammonia nitrogen and TDS had a significant negative correlation with the standing biomass of mollusc community structure. Comprehensive analysis of large-scale commercial sand mining activities, eutrophication of water bodies and construction of water conservancy facilities were key factors threatening the distribution of mollusks in southern Dongting Lake.

Key words: South Dongting Lake, benthic Mollusc, community structure, environment factors

THE IMPACT OF URBANIZATION ON DIATOM COMMUNITY STRUCTURE IN QIANTANG RIVER WATERSHED, CHINA

E. Mbao[1,2], K. Chen[1], J. Gao[1], Y. Wang[1], C. Wu[1], Y.L. Hu[1], L. Sitoki[2], S. Omondi[3], B.X. Wang[1]
[1] Department of Entomology, Nanjing Agricultural University, Nanjing 210095, P.R. China
[2] Department of Geosciences and Environment, The Technical University of Kenya, PO Box 52428-00200 Nairobi, Kenya
[3] Department of Biological Sciences, Egerton University, PO Box 536-20115 Njoro, Kenya

Physicochemical variables are the most widely used parameters for water quality assessment resulting from urbanization activities. However, biological methods particularly diatom assemblages are rapidly being adopted for detecting impact of urbanization. The objective of this study was to examine diatom assemblages' response to water quality and physical variables of streams influenced by different urbanization levels in Qiantang River watershed. Sampling of physicochemical and benthic diatom community data was done in March 2018 in 66 streams within the watershed. We divided the 66 sites into three groups according to the percentages of urban land use at catchment scale: <1%; 1-5% and >5% representing urban 1, urban 2 and urban 3 respectively. Altitude, DO, and depth were significantly higher in urban 1 as compared to urban 2 and urban 3 sites (Kruskal-Wallis one-way ANOVA, $p<0.05$). On the contrary, EC, TDS and salinity were significantly lower in urban 1 as compared to urban 3. Furthermore, our study confirmed that urbanization in the Qiantang watershed was related to the increased levels of COD, TN and TP in the streams. Based on diatom community structure as distinguished by Bray Curtis similarity index, *Achnanthidium minutissimum, Cymbella affinis, Gomphonema parvulum, Navicula lanceolata, Nitzschia palea, Pinnularia brebissonii, Stauroneis anceps f. linearis,* and *Surirella ovalis* were significantly responsible for the differentiation of the 3 urban sites ($p<0.05$). Shannon-wiener and Simpson's diversity indices were significantly higher in urban 1. On the contrary, TDI was significantly higher in urban 3. Our study revealed that TDI, Shannon-wiener, Simpson's diversity, dominant species, % prostrate, % erect, and % stalked were the best biological metrics to predict diatoms response to urbanization.

Key words: benthic diatom, biological metrics, catchment scale, Trophic diatom index

RESPONSES OF MACROINVERTEBRATES AND LOCAL ENVIRONMENT TO SHORT-TERM COMMERCIAL SAND DREDGING PRACTICES IN A FLOOD-PLAIN LAKE

X.L. Meng[1], X.M. Jiang[1], Z.F. Li[1,2], J. Wang[1,2], K.M. Cooper[3], Z.C. Xie[1]
[1] The Key Laboratory of Aquatic Biodiversity and Conservation, Institute of Hydrobiology, Chinese Academy of Sciences, Hubei 430072, China
[2] University of Chinese Academy of Sciences, Beijing 100049, China
[3] Centre for Environment, Fisheries and Aquaculture Science, Lowestoft NR330HT, United Kingdom

In parts of the developing world, the expansion of industrial sand mining activities has led to serious environmental concerns. However, current understanding of the effects of this activity on an inland water ecosystem remains limited. Herein, we choose the "most affected" lake in China (Dongting Lake), to assess the effects of sand dredging on key environmental parameters and on the structure of the macroinvertebrate assemblage. Within the dredged area we observed increases in water depth (on average 2.17 m), turbidity and changes in sediment composition (e.g., increase in % medium sand, and a decrease in % clay). In addition, dredging was associated with a 50 % reduction in taxa richness, Simpson and Shannon-Wiener indices, and a 72 and 99 % reduction in abundance and biomass, respectively. Indirect effects were also observed in the zone surrounding the extraction sites (ca. 500 m), most likely as a result of the dredging processes (e.g., sediment screening and overspill) and water flow. No such effects were observed at a nearby reference site. The direct removal of sediment and indirect alteration of physical conditions (e.g., water depth, turbidity and sediment composition) appear to be the most likely cause of variations in the benthic community. Implications of our findings for the planning, management and monitoring of sand dredging in inland waters.

Key words: Dongting Lake, Aggregate sand dredging, Impacts of sand dredging, macroinvertebrates

PHYTOPLANKTON OF THE MIDDLE PART OF THE AMUR RIVER: SPECIES DIVERSITY, DOMINANT'S CHANGE AND QUANTITATIVE CHARACTERISTICS IN THE SUMMER PERIOD

T.V. Nikulina
Federal Scientific Center of the East Asia Terrestrial Biodiversity, FEB RAS (FSCEATB FEB RAS), 100-letiya Vladivostoka Avenue, 159, Vladivostok, 690022, Russia

The dammed Gassi Lake is located in the territory of the "Anyuisky" National Park (Khabarovsk Territory) and belongs to the largest lakes of the Lower Amur basin. Gassi Lake is a reservoir for 40 species fish spawning and a habitat and reproduction for a relic of East Asia – the Far Eastern tortoise *Pelodiscus maackii* (Brandt, 1857).

The aim of this study is to reveal species diversity of periphyton algae on Gassi Lake and to assess the lake water quality.

The famous Russian researcher B.V. Skvortsov (1917, 1918) began to study the species diversity of algae in the lake systems of the Lower Amur. The first data on plankton algae of Gassi Lake are known from paper by A.G. Khakhina (1937). Later, the species diversity of algal flora on the lake was examined by E.V. Borutsky (1952).

The species composition of the periphyton algae of Gassi Lake is represented by 174 species (183 intraspecies taxa) from the divisions Cyanobacteria, Bacillariophyta, Chlorophyta, Rhodophyta, Euglenozoa, and Myzozoa. Within the algal flora systematic structure the division Bacillariophyta contains the largest number of species, varieties and forms, and makes up 83.6 % of the total number of species. The class Bacillariophyceae is most diverse; it includes 114 intraspecies taxa (64.5 % of all algae taxa). The genera *Pinnularia* (16 intraspecific taxa), *Gomphonema* (13) *Nitzschia* (12), *Navicula* (11), *Eunotia* (8), *Surirella* (8), and *Aulacoseira* (7) contain the greatest number of species and varieties and are classified as leading. In periphyton communities diatom species *Cymbella tumida*, *Gomphonema truncatum* were dominants, and *Aulacoseira subarctica*, *Tabellaria flocculosa,* and *Surirella minuta* were subdominants in June 2017; *Aulacoseira subarctica* is dominant in July 2017; *A. subarctica* is dominant, and *A. ambigua* is subdominant in August 2017.

Two rare diatom species from genera *Surirella* – *S. pantocsekii* Meister and *S. tientsinensis* Skvortzow were characterized by its East-Asian distribution; they were found in the reservoirs of Honshu, Moneron and Onekotan islands, the Primorye Territory, and the Amur River basin (Skvortzow, 1931, 1936, 1938; Medvedeva, Nikulina, 2014, et al.)

General analysis of the algal flora from Gassi Lake showed that most species are benthic (66.1 % of the total number of identified species); in relation to salinity most species would be classified as indifferent (60.7 %); in relation to the pH, the alkaliphil species were most common (36.6 %), and indifferent (20.2 %). Oligo- and betamesosaprobionts were the most representative indicators of water saprobity (33.9 and 26.8 %, respectively).

Key words: Amur River, Gassi Lake, periphyton algae, species diversity, Bacillariophyta

WEATHER, LAND COVER AND ANTHROPOGENIC IMPACT ON MOSQUITO POPULATION DYNAMICS IN CHIANG MAI CITY, THAILAND

P. Rahong[1], C. Techakijvej[1], N. Sarein[3], Y.J. Bae[3], C. Phalaraksh[1,2]
[1] Environmental Science program, Faculty of science, Chiang Mai University, Chiang Mai, 50200 Thiland
[2] Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand
[3] Department of Environmental Science and Ecological Engineering, Korea University, Seoul 02841, Korea

The understanding of mosquito population and influence factors that effect on their population are very important, especially in the big city that reported the mosquito-borne disease outbreak. Over 3,520 mosquito species that recognized in the world and 459 species in Thailand. Many species of mosquito were transmitted serious disease-causing viruses or parasites. In 2017, there have been 50,033 patients that infected with the dengue virus and 59 died, which accounts for around 0.1% of those affected (Bureau of vector borne diseases, 2017). In Chiang Mai city (Mung District) was reported 554 patients that the first rank of dengue fever in last year.

Digital Mosquito Monitoring System (DMS, Environmental Technology & Development: E-TND) is tools for monitor mosquito population by using carbon dioxide gas diffused for attached mosquito. Data were collected from 2 machines in every hour and the number of mosquito were counted by using LED ray sensor. Mosquito data were represent mosquito population in winter season and hot season of Thailand. The *Aedes* and *Culex* genera were the most species that found in sampling area, which including in important vector born disease. Monitoring system reported high accuracy efficiency of automatic mosquito counting. Climate data were got from nearest meteorological station of DMS machine (e.g., maximum temperature, minimum temperature, precipitation, humidity and wind speed). Moreover, land used and anthropogenic impact data were analyzed by using Geographic Information System (GIS) and observation from people in sampling area.

From the result shown the correlations between some parameter in climate data, land used and human activities time with mosquito dynamics population in each day on both season. The understanding of population dynamic and relation with other factors can be one of the solutions for mosquito control.

Key words: population, mosquito, dynamic, climate and anthropogenic impact

EFFECTS OF FLOOD DISTURBANCE ON COHORT STRUCTURE OF RIVERINE MAYFLY *EPHEMERA ORIENTALIS* (EPHEMEROPTERA: EPHERMERIDAE) IN THE HAN RIVER IN SEOUL, KOREA

S.W. Seok[1], M.J. Baek[2], J.M. Hwang[3], S.H. Park[1], Y.J. Bae[1,3]
[1] Department of Environmental Science and Ecological Engineering, Korea University, Seoul, Korea
[2] KIST-Europe, Saarbrücken, Germany
[3] Korean Entomological Institute, Korea University, Seoul, Korea

A flood is one of the major damaging natural events for aquatic insects and, therefore, aquatic insects adapt their morphology, behavior, and life history to avoid floods. Life history and cohort structure of the riverine mayfly *Ephemera orientalis* (Ephemeroptera: Ephemeridae) were studied to elucidate how they adapt their life history at the cohort level in response to floods. From March 2012 to November 2014, we collected larvae of *E. orientalis* quantitatively once or twice month from the Godeok-dong, the Han River, Korea using a Surber sampler (50 cm x 50 cm, mesh 0.25 mm). A size-frequency method using head capsule width was employed for cohort separation. We took the daily precipitation data from Korea Meteorological Administration as a flood indicator, and conducted regression analysis to determine the relationships between relative cohort size and the number of flood occurrences. To define the flood season, threshold functions of discharge were calculated. We compared our results with those of research conducted in 2006, when an unusually severe flood occurred. Our study showed that two slow-growing cohorts (S1 and S2 cohorts) and one fast-growing cohort (F cohort) occur in the Han River. The S1 cohort hatchs in July and emergs in the mid May to June of the following year, while the S2 cohort hatchs in August to September in one year and emerges in August the next year. Early hatched larvae of the S1 cohort become the F cohort that emergs with the S2 cohort in August. It is inferred that high summer temperatures lead to the development of the F cohort by cohort splitting, knwon as initiation asynchrony. The F cohort was not found in 2006, when the severe flood occurred. The high precipitation in 2006 may result in low water temperatures, which were not sufficient for development of the F cohort. In addition, the flood significantly reduced the relative cohort size. Therefore, floods are not only directly disturbing to *E. orientalis*, but they also have an indirect effect by lowering the water temperature. All cohorts emerge before or after the flood season (July 10 to August 10), and this phenomenon shows that *E. orientalis* has adapted its their life history to avoid the flood season.

Key words: flood effect, life history, cohort structure, cohort splitting, *Ephemera orientalis*, Han River

METACOMMUNITY STRUCTURE OF BENTHIC MACROINVERTEBRATES VARIES BETWEEN AUTUMN AND WINTER IN POYANG LAKE CATCHMENT

C.Z. Tan, C. Wu, J. Gao, R. Fu, B.X Wang
Department of Entomology, Nanjing Agricultural University, Nanjing 210095 P.R. China

Metacommunity provides new perspective on temporal and spatial variation of regional communities. Seasonal hydrology dynamics of Poyang Lake, the Chinese largest river-connected lake, result in great landscape variation between wet and dry seasons. Do metacommunity structures of benthic macroinvertebrate vary in accordance with the distinctive hydrological cycle are not clear. In this study, we aimed to examine the variation of metacommunity structure of benthic macroinvertebrates between October 2017 and January 2018 using elements of metacommunity structure (EMS) approach. We sampled macroinvertebrates from the lake, rivers and ponds in Poyang Lake catchment, with a total of 43 sites in October and 39 sites in January. A total of 143 taxa were collected, ranging from 2 to 37 taxa per sample. Among them, there are 65% taxa in Arthropoda, 30% taxa in Mollusca, and 5% taxa in Annelida. The five most commonly occurring taxa during two months were *Glyptotendipes*, *Tanytarsus*, Oligochaeta, *Bellamya purificata*, and *Parafosarulus eximius*. The EMS analysis revealed that in October the Quasi-nestedness with clumped species loss was the best fit the metacommunity structure, and in January, the pattern that best characterized the metacommunity structure was Clementsian. Our preliminary result indicated the temporal metacommunity structures may highly be related to the hydrological variation.

Key words: metacommunity structure, benthic macroinvertebrates, Poyang lake catchment, seasonal hydrology dynamics

DIVERSITY OF BENTHOS IN GANJIANG RIVER AND ITS CORRELATION WITH ENVIRONMENTAL FACTORS

Y. Xing, Z.C. Xie
The Key Laboratory of Aquatic Biodiversity and Conservation, Institute of Hydrobiology, Chinese Academy of Sciences, 7 Donghu South Rd., Wuhan 430072, Hubei, China

To examine longitudinal patterns of microbenthic biodiversity of Ganjiang River, macrozoobenthos community structure in the GanJiang River was investigated in October 2016 to August 2017. This river harbored a total of 227 taxa belonging to 5 phyla, 8 classes and 77 families. Among them, insecta was the species-richest group (158 taxa),followed by Oligochaeta (29), Mollusca (23) and Leech (8) . In the branches of the middle and lower GanJiang River, Species richness, biomass, Margalef and Shannon diversity exceed that in the mainstream and the tributaries located in the upstream areas. CCA analysis showed that two environmental factors (river width and flow velocity) and two spatial factors (PCNM1 and PCNM4) were the key drivers structuring the microbenthic communities. Variance partitioning analysis indicated that the environmental factors had a stronger controlling effect on microbenthic communities than spatial ones. The study provides useful information for the conservation of benthic biodiversity in GanJiang River.

Key words: community structure, GanJiang River, macrobenthos

RELATIONSHIP BETWEEN MACROPHYTE COMMUNITIES AND MACROINVERTEBRATE COMMUNITIES IN AN URBAN STREAM

Y. Yu, X.D. Qu, M. Zhang, H.P. Zhang
Water Environment Institute, China Institute of Water Resources and Hydropower Research, Beijing

The channelization has caused severe degradation of aquatic ecosystems during the past decades of rapid urbanization in metropolitan areas of China. The reconstruction of the in-stream habitat of aquatic organisms and the restoration of aquatic ecosystems were more difficult in the urban stream than in the natural stream with the effluence of nutrient enrichment, water contamination, and in-stream habitat loss. Considering the ecological effects of the submerged macrophyte replantation on macroinvertebrate communities, one of the urban streams that used replantation restoration strategy was seasonally monitored from October 2012 to July 2013. There were four sampling sites, two located at the upper region and two in the middle region. Due to the relatively high levels of organic matter contamination, there are no sites in the downstream region of Qinghe River. Four types of submerged macrophyte were planted at each site to restore the in-stream habitat of two years ago, including *Potamogeton pectinatus*, *Potamogeton crispus*, *Hydrilla verticillate*, and Ceratophyllum demersum. Because of the unexpected development, *Myriophyllum spicatum* and *Acorus calamus* appeared at the upper reach of Qinghe River. Considering the average water depth of 30-40 cm, the revised Surber net with the enlarged net was used to collect macroinvertebrate samples. At each sampling site, three replicates of macroinvertebrates were carefully collected for each type of macrophyte. Three replicates were sampled for the comparison at the imperviously concrete sections of each site. The community composition of the macroinvertebrate was determined by cluster analysis and ordination analysis. The density, biodiversity, and community stability were higher in the sampling sections with the replantation of macrophyte than in impervious concrete sections. The occurrence of intermediate tolerant taxa such as *Ephemera* sp., *Caenis sinensis* Gui, *Ecnomus* sp., and *Hydropsyche* sp. indicated the recovery and restoration of macroinvertebrates in Qinghe River. However, the differences in the community structure, density, taxa richness, biodiversity index, and the composition of functional feeding groups of macro-invertebrates among different types of submerged macrophyte were not identified. Unlike providing extra habitats for macroinvertebrates in the vertical direction in natural streams and lakes, the submerged macrophyte provided more stable benthic habitats in urban streams. The stem and leaf of macrophytes could adjust the hydraulics and continually absorb, fix, and accumulate the suspended solids in the sediment and water interface. The root systems could stabilize the microhabitat of the sediment for macroinvertebrates, benthic algae, and microorganisms. Those aquatic organisms played an important role in the decomposition, transformation, and mineralization of nutrients and organic matter in urban streams. Following the recovery of stabilized microhabitats, community restoration and secondary succession of macroinvertebrates could continually and slowly happen. This study improved the understanding of the ecological effects of macrophytes on the

restoration of aquatic organisms and ecosystems in urban streams.

Key words: macroinverte, macrophyte replantation, ecological restoration, urban stream, microhabitat

POSTER SESSION

ABSTRACTS

Poster Session | S01

METACOMMUNITY ECOLOGY MEETS BIOASSESSMENT: ASSESSING SPATIO-TEMPORAL VARIATION IN MULTIPLE FACETS OF MACROINVERTEBRATE DIVERSITY IN HUMAN-INFLUENCED LARGE LAKES

Y.J. Cai[1,2], Y. Zhang[1], Z.X. Hu[2,3], J.M. Deng[2], B.Q. Qin[2], H.B. Yin[2], Z.J. Gong[1,2], X.L. Wang[1,2], J. Heino[4]

[1] Key Laboratory of Watershed Geographic Sciences, Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences, Nanjing 210008, China
[2] State Key Laboratory of Lake Science and Environment, Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences, Nanjing 210008, China
[3] School of Environmental Engineering, Nanjing Institute of Technology, Nanjing 211167, China
[4] Finnish Environment Institute, Biodiversity Centre, Paavo Havaksen Tie 3, FI-90570 Oulu, Finland

Metacommunity theory emphasizes that local communities are jointly affected by environmental filtering and spatial processes. However, the roles of spatial processes are generally ignored in bioassessment practices, which may bias the assessments of ecological status based on biotic metrics. Here, we quantified the relative importance and the seasonal stability of spatial processes, natural factors and human disturbance in structuring variation in different bioassessment metrics based on macroinvertebrate communities. Our study systems were two extensively sampled large and shallow lakes with strong nutrient gradients related to human disturbance. The roles of different drivers were examined for three kinds of indicators: general diversity, trait-based and taxonomic distinctness metrics, and their performance in characterizing human disturbance was evaluated. Overall, the three groups of drivers were all important in explaining variation in the bioassessment metrics. Contrary to our expectations, however, we found that the importance of spatial processes on bioassessment metrics can be comparable to the effects of local environmental conditions at the within-lake scale. Furthermore, the results showed substantial seasonal variability in the relative roles of different drivers, which might be linked to life-cycle seasonality of macroinvertebrates. As expected, trait-based metrics generally were best associated with human disturbance variables in both lakes, whereas general diversity and taxonomic distinctness metrics performed poorly. The low effectiveness of taxonomic distinctness metrics might due to low species richness associated with high nutrient levels. To conclude, our results suggest that bioassessment cannot exclusively rely on the idea of environmental filtering even if we focus on fine spatial extents. We hence strongly urge that spatial processes, natural drivers and temporal variability should be better considered in combination in the development and application of bioassessment approaches. In addition, taxonomic distinctness measures should be used with caution, especially for the ecosystems and organism groups typically characterized by low species richness.

SPECIES DETECTION PERFORMANCE OF MACROINVERTEBRATES USING ENVIRONMENTAL DNA METABARCODING BETWEEN WATER SAMPLES AND ETHANOL SAMPLES

Y. Wang, B.X. Wang, J. Gao
Department of Entomology, Nanjing Agricultural University, Nanjing 210095 P.R. China

Species detection using environmental DNA (eDNA) of water samples is increasingly recognized a fast and efficient method for species richness survey of aquatic macroinvertebrates. However, less attempts are made on the ethanol from field preserved macroinvertebrate samples. Due to the strong mobility of stream, the water sample of a specific site may result in a false positive effect on the true species richness, and ethanol samples assumed to take the advantage of water directly sampled from the running stream. In this study, we aimed to examine the performance of eDNA metabarcoding in species detection of macroinvertebrates between the water samples and the ethanol samples. Two kind of samples were collected from 14 stream sites simultaneously in Qiantang River Basin, April 2018. DNA was extracted from each glass microfiber filter after filtering a sample, then amplified by targeting fragments of the cytochrome c oxidase subunit I (COI) gene to acquire the metabarcodes for bioinformatic analysis. These samples were amplified successfully except for two water samples. A total of 676 and 663 macroinvertebrate molecular operational taxonomic units (MOTUs) were obtained for water and ethanol samples, respectively. Ethanol samples offered more effective sequences and were able to identify more genus and species than water samples. Compared with 24.0% of the MOTUs in ethanol samples, only 17.2% of the MOTUs for water samples could be identified to the species or genus level, although no significant difference in MOTUs detected by two kind of samples at each site ($p>0.05$). Our results suggested that the ethanol sample is a potential alternative for species detection of macroinvertebrates though most of MOTUs can only be identified to family or coarser resolution due to the lack of regional DNA barcode database.

Key words: eDNA; macroinvertebrates; high throughput sequencing; stream; biodiversity

MACROINVERTEBRATE BIODIVERSITY IN RELATION TO ENVIRONMENTAL VARIABLES OF LITTORAL ZONE IN THE LOWER YANGTZE RIVER FROM NANJING TO THE ESTUARY

C. Wu[1], J. Xu[2], S.L. Yin[2], C.Z. Tan[1], K. Chen[1], J. Gao[1], B.X. Wang[1]
[1] Department of Entomology, Nanjing Agricultural University, Nanjing 210095 P.R. China
[2] Chinese Research Academy of Environmental Sciences Beijing 100012, China

Macroinvertebrates are potential surrogates for freshwater biodiversity and their relationships with environmental variables provide valuable information for biodiversity conservation. Here, we conducted a survey on littoral zone macroinvertebrate, water quality and physical variables of 43 sites from 6 sections along lower Yangtze River Channel from Nanjing to estuary in April 2017, and aimed to evaluate the macroinvertebrate biodiversity and explore the potential drivers. A total of 63 taxa belonging to 35 families, 17 orders, 7 phylums and 3 classes were recorded and Athropoda and Mollusca were dominant group and *Limnodrilus* sp. was the dominant species. Interestingly, the *Dentinephtys glabra*, previously recorded in the estuary only, became a common species of nereid from sections of Nanjing to estuary. In terms of the species richness and Shannon-Wiener index among 6 sections, Zhenjiang had the highest richness of 31 and diversity index of 1.71, followed by Jiangyin, and the north branch of estuary had the lowest richness of 12 and diversity index of 0.90. CCA results showed that water pollution, habitat degradation or loss and shipping were the major factors influencing the macroinvertebrate assemblage in the lower Yangtze River channel. We suggested the water pollution control and habitat restoration were two important means in the conservation of macroinvertebrate diversity in the lower Yangtze River channel.

Key words: Mollusca, Nereid, water quality, physical habitat, biodiversity conservation

IMPROVING THE MACROINVERTEBRATE-BASED BI CLASSIFICATION CRITERIA FOR WATER QUALITY ASSESSMENT IN ZHENGJIANG PROVINCE, EASTERN CHINA

J.W. Zhang, K. Chen, S.W. He, B.X. Wang
Department of Entomology, Nanjing Agricultural University, Nanjing 210095 P.R. China

Biotic Index (BI) has been used in aquatic health assessment worldwide, as BI is sensitive to organic pollution and nutrients contaminations. It is critical to establish specific BI classification criteria by eliminating boundary confusion for regional health of aquatic ecosystems assessment. We developed a regional macroinvertebrate-based BI health classification and evaluated its performance for stream and river conditions assessment in the Zhejiang Province, eastern China. We determined least-disturbed and most-degraded condition using a *priori* screening criteria. The BI values responded linearly along the comprehensive environmental gradients from values of first axis of principal component analysis. We used a statistical quantile method to develop two BI health classification criteria using 75th percentile of BI values across least disturbed sites and 5th percentile of BI values across all sites, as sites with BI values in excellent and good classes as biologically undegraded and in poor and bad classes as biologically degraded condition. We compared the performance of the BI health classification criteria in terms of sensitivity (the proportion of biologically degraded sites were in physicochemical most-disturbed conditions) and specificity (the proportion of biologically undegraded were in physicochemical least-disturbed conditions). The results showed that sensitivity and specificity were 52.38% and 91.40% when 75th percentile classification method used, and 66.01% and 92.97% when 5th percentile classification system used. We recommend using BI health classification criteria from 5th percentile across all sites to assess pollution conditions in streams and rivers in the Zhejiang Province, eastern China.

Key words: percentile method, health criteria classification, performance, sensitivity and specificity

Poster Session S02

SOME DATA ABOUT MACROZOOBENTHOS IN LITTORAL ZONE OF ARCTIC LAKES OF THE PUTORANA PLATEAU, KRASNOYARSK REGION, RUSSIA

L.V. Bazhina[1], K.A. Semenchenko[2], V.O. Kleush[1]
[1] Scientific Research Institute of Ecology of Fishery Reservoirs, Pariskoy Kommunii street, 33, Krasnoyarsk 660049 Russia
[2] Institute of Biology and Soil Science FEB RAS, 159 Stoletiya Vladivostoka Ave., Vladivostok, Russia

In August-September, 2013-2014 researches of benthic macroinvertebrate communities of Large Norilsk lakes (Lama Lake and Sobach'e Lake of the Pyasina river basin) and of the Kutaramakan Lake, located in the western part of the Putorana plateau, were conducted (of the Yenisei basin). In general, 64 taxons of invertebrates (from 13 group) are found in benthos, from them 42 taxons by *Chironomidae*, 5 – water mites, 3 – the rest *Diptera*, 3 – *Oligochaeta*, 2 – *Amphipoda*, 2 – *Mollusca*. One species of invertebrates is found in each of such invertebrate groups as *Coleoptera*, *Thichoptera*, *Plecoptera*, *Nematoda*, *Hirudinea*, *Ostracoda* and *Podura*. Five species of water mites (*Hydrachnidia*): *Acalyptonotus violaceus* Walter, *Hygrobates (Hygrobates) foreli* (Lebert), *Lebertia (Mixolebertia) densa* Koenike, *Lebertia (Pilolebertia) porosa* Thor, *Oxus (Gnaphiscus) setosus* (Koenike) were described for the first time in that territory. The representatives of *Chironomidae* family, as *Monodiamesa* group *bathyphila*, *Protanypus caudatus*, *Heterotrissocladius* group *marcidus*, *Sergentia* group *coracina* and *Tanytarsini* spp. were often found in the Pyasina river basin, while such as *Orthocladius* group *saxicola*, *Sergentia* group *coracina*, *Procladius* group *ferrugineus* and *Tanytarsini* spp. were often found in the Yenisei river basin. Attention is drawn to the lack of *Amphipoda* in the Kutaramakan Lake of the Yenisei basin. On the average for all lakes, the values of Shannon-Weaver Index are 2.21±0.31, that corresponds to oligotrophic water body (Alimov, 2001). In the zone protected from excitement, deeper than 2.5 meters, on the silty and silty-sandy soils of Sobach'e Lake, bottom communities of invertebrates reach the greatest quantitative development, in average here a maximal density is 2510/m^2, a biomass – 4.58 g/m^2. By a biomass of a zoobentos, Lama Lake (1.20±0.32 g/m^2) and Kutaramakan Lake (1.09±0.72 g/m^2) can be attributed to an ultraoligotrophic type. Among the studied lakes, the Sobach'e Lake differs in the greatest average biomass of a zoobenthos – 3.85±0.69 g/m^2, this corresponds to α-mezotrofic type.

Key words: zoobenthos, lake, Lama, Sobach'e, Kutaramakan

DISTRIBUTION OF DECAPOD CRUSTACEANS IN THE TRUONG GIANG RIVER, QUANG NAM PROVINCE, VIETNAM

X.N. Ngo[1], N.H. Nguyen[1], V.V. Nguyen[2]
[1] Institute of Ecology and Works Protection, 267 Chua Boc Street, Dong Da District, Hanoi, Vietnam
[2] Faculty of Biology, VNU University of Science, 334 Nguyen Trai, Thanh Xuan, Hanoi, Vietnam

Samples of Decapod crustaceans were obtained along Truong Giang river, Quang Nam province, from 2016 to 2018. A total of 30 species were identified, belonging to 16 genera of 9 families, and including 23 species of of Brachyura, 7 of Macrura. Decapod crustaceans were collected in brackish and freshwater areas, which varied considerably between Brachyura and Macrura. Only one species of freshwater crab (*Somanniathelphusa* sp.) was recorded. Meanwhile, 5 freshwater species of Macrura (*Caridina acuticaudata*, *Caridina subnilotica*, *Caridina* sp., *Macrobrachium nipponense*, *Macrobrachium* sp.) were recorded. Brachyura were distributed from medium-brackish water to brackish-salt water water (4 - 25‰), while Macrura recorded from fresh-brackish water to light brackish water (0.2 - 4‰). There may be isolation of populations of brackish species in the two parts of the river. Brackish species are widely distributed, tropical species and belonging to Indo-West Pacific region.

Key words: Decapod crustaceans, distribution, brackish, freshwater, Truong Giang river

SPECIES DIVERSITY OF PERYPHYTON ALGAE FROM THE GASSI LAKE (THE LOW AMUR RIVER, RUSSIA)

T.V. Nikulina
Federal Scientific Center of the East Asia Terrestrial Biodiversity, FEB RAS (FSCEATB FEB RAS), 100-letiya Vladivostoka Avenue, 159, Vladivostok, 690022, Russia

The dammed Gassi Lake is located in the territory of the "Anyuisky" National Park (Khabarovsk Territory) and belongs to the largest lakes of the Lower Amur basin. Gassi Lake is a reservoir for 40 species fish spawning and a habitat and reproduction for a relic of East Asia – the Far Eastern tortoise *Pelodiscus maackii* (Brandt, 1857).

The aim of this study is to reveal species diversity of periphyton algae on Gassi Lake and to assess the lake water quality.

The famous Russian researcher B.V. Skvortsov (1917, 1918) began to study the species diversity of algae in the lake systems of the Lower Amur. The first data on plankton algae of Gassi Lake are known from paper by A.G. Khakhina (1937). Later, the species diversity of algal flora on the lake was examined by E.V. Borutsky (1952).

The species composition of the periphyton algae of Gassi Lake is represented by 174 species (183 intraspecies taxa) from the divisions Cyanobacteria, Bacillariophyta, Chlorophyta, Rhodophyta, Euglenozoa, and Myzozoa. Within the algal flora systematic structure the division Bacillariophyta contains the largest number of species, varieties and forms, and makes up 83.6 % of the total number of species. The class Bacillariophyceae is most diverse; it includes 114 intraspecies taxa (64.5 % of all algae taxa). The genera *Pinnularia* (16 intraspecific taxa), *Gomphonema* (13) *Nitzschia* (12), *Navicula* (11), *Eunotia* (8), *Surirella* (8), and *Aulacoseira* (7) contain the greatest number of species and varieties and are classified as leading. In periphyton communities diatom species *Cymbella tumida*, *Gomphonema truncatum* were dominants, and *Aulacoseira subarctica*, *Tabellaria flocculosa,* and *Surirella minuta* were subdominants in June 2017; *Aulacoseira subarctica* is dominant in July 2017; *A. subarctica* is dominant, and *A. ambigua* is subdominant in August 2017.

Two rare diatom species from genera *Surirella* – *S.pantocsekii* Meister and *S. tientsinensis* Skvortzow were characterized by its East-Asian distribution; they were found in the reservoirs of Honshu, Moneron and Onekotan islands, the Primorye Territory, and the Amur River basin (Skvortzow, 1931, 1936, 1938; Medvedeva, Nikulina, 2014, et al.)

General analysis of the algal flora from Gassi Lake showed that most species are benthic (66.1 % of the total number of identified species); in relation to salinity most species would be classified as indifferent (60.7 %); in relation to the pH, the alkaliphil species were most common (36.6 %), and indifferent (20.2 %). Oligo- and betamesosaprobionts were the most representative indicators of water saprobity (33.9 and 26.8 %, respectively).

Key words: Amur River, Gassi Lake, periphyton algae, species diversity, Bacillariophyta

SEASONAL DYNAMICS OF MACROINVERTEBRATE COMMUNITY STRUCURE IN A HEADWATER STREAM IN THE CHANGBAI MOUNTAINS

L. Wang, H.J. Yang, C.L. Lin, G. Chen, Y.W. Liu, Y.W. Gong, Y. Tan
Key Laboratory of Vegetation Ecology, Northeast Normal University, Changchun, 130024, China

Headwater streams are critical locations with nutrient recycling and energy flow along a river ecosystem, posing vital significance to macroinvertebrate biodiversity maintenance in rivers. However, in China, research upon headwater streams' macroinvertebrate biodiversity community structure is few, and the report about seasonality of macroinvertebrate community structure in headwater streams of the Changbai Mountains is particularly lacking. By using in-situ sampling in the wild, we attempt to elucidate seasonality of river macroinvertebrates and the major environmental drivers behind in headwater streams of the Changbai Mountains. The results revealed: (1) A total of 90 taxa of river macroinvertebrates were identified, pertaining to 3 classes, 9 orders, and 38 families. Among which, aquatic insects (85 genera) were dominant. Seasonality of the river macroinvertebrates' community structure was manifest, with density and diversity of the macroinvertebrates significantly higher in fall and summer than in winter and spring, reaching minimums in winter. (2) Gather-collectors were dominant functional feeding groups, and then shredders, predators, and scrapers. By contrast, filter-collectors accounted for a litter part. In terms of habit trait groups, clingers were the dominant group, and then swimmers and burrowers, sprawlers and climbers accounted for a litter part. The seasonality of different functional feeding groups and different habit trait groups all indicated not in line with each other, despite density and species richness all demonstrated highest in autumn. (3) water temperature, distribution of leaf litter, and flow velocity were major drivers of seasonal dynamics of river macroinvertebrate communities in the area. Our results may provide a support for addressing the headwater streams ecology in the Changbai Mountains, and ecological restorations of the Songhua River basins.

Key words: The Changbai Mountains, macroinvertebrate, seasonal dynamics, functional feeding groups, habit trait groups

Poster Session | S03

EFFECTS OF HUMAN ACTIVITIES ON MACROZOOBENTHOS IN GUAN RIVER BASIN OF DANJIANGKOU RESERVOIR AREA

X.M. Han[1,2], X.M. Yang[1], S.J. Guo[1,2], Y.Y. Li[1,3]
[1] Henan Key Laboratory of Ecological Security for Water Source Region of Mid-line of South-to-North Diversion Project of Henan Province, Collaborative Innovation Center of Water Security for Water Source Region of Mid-line of South-to-North Diversion Project of Henan Province, Nanyang Normal University, Nanyang 473061, China
[2] School of Life Science and Technology, Nanyang Normal University, Nanyang, China
[3] College of Agriculture Engineering, Nanyang Normal University, Nanyang, China

Farmland excessive uses and frequent human activities have caused nitrogen content increases and the eutrophication in rivers, which also influenced macrozoobenthos` community structures. The water quality and the macrozoobenthos` communities under four land use types were analyzed in Guan River basin of Danjiangkou reservoir area of Mid-line of South-to-North Diversion Project. The four land use types are: 1) The forest coverage > 90%; 2) The forest coverage > 50%, and the resident and farmland coverage < 50%; 3) The forest coverage < 50%, and the resident and farmland coverage > 50%; 4) The resident and farmland coverage > 90%. On the basis of the tributary basin area, and the spatial distribution of mainstreams and tributaries, and the upstream and the downstream, a total of 35 sampling points are conducted. The water and biological samples were collected in March (the low water period), June (the normal water period), September (the high water period) and December (the low water period) in each year. The on-the-spot testing indicators included the water temperature, the pH value, DO, COND and ORP. The lab testing indicators included total phosphorus, total nitrogen, ammonia nitrogen, nitrate nitrogen, nitrite nitrogen, COD and chlorophyll. Macrozoobenthos were collected semi-quantitatively using the D-shaped trawl, which were identified to species or genera.

Preliminary analysis showed that the total nitrogen contents gradually increased with the increases of human activities and the farmland coverage. In March 2018, a total of 5,987 macrozoobenthos were collected, which distributed in 27 species, 6 orders and 4 phyla. There are 8 species of Mollusca (17.8%), 2 species of Annelida (9.1%), and 2 species of the Arthropoda (73.1%). The dominant families was Baetidae, which occupied 17.2%. With the increase of human activities, the anti-pollution types of macrozoobenthos gradually increased, but they distributed irregularly from the upstream to the downstream, which indicated that the tributaries had the function of purify the main streams. According to the macrozoobentho distribution, the water quality of Guan River was good. Their community distribution were consistent with the change of physico-chemical parameters. The research provides a scientific basis for the health evaluation of the ecological system of the Guan River basin, the establishment of the ecological database of water source region of Mid-line, the ecological restoration of this region and the government scientific decision-making.

BENTHIC MACROINVERTEBRATE COMMUNITY DISTRIBUTION IN RESERVOIR AND UNDER DAM OF YULIANG SHIPPING HUB IN YOU RIVER GUANGXI PROVINCE

H.L. Wang[1,3,4], H.T. Li[2,3], N. Li[2,3], M. Tao[2,3], H.W. Zhang[2,3], Q. Wang[4], X. Xu[2,3], Q.H. Zhang[1,3], S. Shu[2,3]

[1] Institute of Aquatic Ecosystem Conservation of the Yangtze River, Hubei Province
[2] Wuhan Sinoeco Ecological, Science & Technology Co., Ltd. Wuhan, 430080, China
[3] Engineering Research Center of Conservation and Restoration of Aquatic Biodiversity, Hubei Province
[4] Wuhan Sinoeco Testing technology Co., Ltd. Wuhan, 430080, China

The spatial-temporal distribution of benthic macroinvertebrate in reservoir and under dam of Yuliang shipping hub in You River Guangxi Province had been investegated in June and September 2017. Both had four sampling stations distributed along the river in reservoir and under dam, respectively. 22 species of macrobenthos were identified in the sampling sites and they were belong to 18 genus, 14 families, 6 class, 3 phylum. During this survey, 9 indicators of polluted environment were found, they were *Glossiphonia sp., Limnodrilus hoffmeisteri*, *Branchiura sowerbyi, Corbicula fluminea, Radix sp. Radix swinhoei, Oophana heudei, glabra, Dicrotendipes sp*. According the cluster analysis of benthic macroinvertebrate community in software Primer 5, there were no differences between the reservoir and under dam but the seasonal variation between June and September was apparent. The main taxa in June were *Limnoperna lacustris, Bellamya sp., Corbicula fluminea, Pleuroseridae, Caridina sp.* and *Dicrotendipes sp*. Whatever in September were *Limnoperna lacustris, Bellamya sp. Limnodrilus hoffmeisteri,* and *Thiaridae*. There were no differences in number of indicators of polluted environment in spatial and temporal in Yuliang shipping hub area. Thus, benthic macroinvertebrate community distributed variated largely with season but not spatial. Moreover, the water in this section both reservoir and underdam in June and September were all contaminated to some extent without differences between spatial and temporal.

Key words: benthic macroinvertebrate, spatial-temporal, Yuliang shipping hub

Poster Session S04

CONSTRUCTION OF REGIONAL DNA BARCODE LIBRARY OF MOLLUSCA IN YANGTZE RIVER DELTA

R. Fu, B.X. Wang, K. Chen
Department of Entomology, Nanjing Agricultural University, Nanjing, 210095, P.R. China

The DNA barcoding as a biodiversity assessment tool receives increasing attention for its potential of a rapid and relatively unbiased prospecting in biodiversity survey. Establishment of a sound regional specific species-pool-based DNA barcode library is able to provide a great basis and reference for long-term regional biodiversity monitoring and conservation activities. The Yangtze River Delta, located in lower Yangtze River basin eastern China, suffered from heavy human activities (e.g. water pollution and land use development) and serious biodiversity degradation. To complete a full understanding of known mollusca biodiversity in the Yangtze River Delta, we attempted to obtain DNA barcodes of aquatic gastropods and bivalvia, and then to build up their DNA barcode library. We obtained DNA barcodes through DNA extraction, PCR amplification, and sequencing using COI gene 658 bp of morphologically identified species. The obtained sequences were further individually compared against the NCBI GenBank and BOLD systems using BLAST for verification using a 99% similarity cutoff. Currently, we have obtained DNA barcodes of 7 gastropods species and 13 bivalvia species in Yangtze River Delta, including 16 barcodes corresponding to the NCBI GenBank and BOLD systems, and 4 new records.

Key words: benthic macroinvertebrates, biodiversity, DNA barcoding, water

DESCRIPTIONS OF LARVAE OF FIVE PHILOPOTAMIDAE SPECIES FROM CHINA (INSECTS, TRICHOPTERA)

Y.L. Hu, B.X. Wang, C.H. Sun, L. Peng, Y. Wang
Department of Entomology, Nanjing Agricultural University, Nanjing, 210095, P.R. China

The Philopotamidae Stephens, 1829 is divided into 3 subfamilies, including 20 genera and about 1300 known species around the world so far, however only about 55 larval stages were described or illustrated in the five genera: *Chimarr*a Stephens 1829, *Wormaldia* McLachlan 1865, *Dolophilodes* Stepens 1829, *Gunungiella* Ulmer 1913 and *Kisaura* Ross 1956. In China, the Philopotamidae includes 2 sufamilies, represented by above mentioned 5 genera, with a total of 82 known species, however no larvae was known. In this study, we described five species of larvae, representing four genera collected from Zhejiang Province, China. The larvae of 5 species were successfully associated with males by mtCOI gene sequences. They are *Chimarra paramonorum* n. sp., *Chimarra sadayu* Malicky 1993, *Dolophilodes bellatula* Sun & Malicky 2002, *Wormaldia unispina* Sun 1998 and *Kisaura* sp., of which the larva of geneus *Kisaura* was described for the first time in Philopotamidae. In addition, we provide a key to the four genera of the larvae of Chinese Philopotamidae.

Key words: taxonomy, Trichoptera, larva, DNA barcoding, morphology

TWO NEW RECORDS OF LEUCTRIDAE (PLECOPERA) FROM SOUTH KOREA

J.M. Hwang[1], D. Muranyi[2], J.H. Kang[1], S.W. Seok[3], S.W. Park[3]
[1] Korean Entomological Institute, Korea University, Seoul 02842, Korea
[2] Department of Zoology, Hungarian Natural History Museum, Baross u. 13, H-1088 Budapest, Hungary
[3] Division of Environmental Science and Ecological Engineering, Korea University, Seoul 02842, Korea

The family Leuctridae Klapálet is a relatively small taxon of insects with approximately 350 species in the world. However, only 15 species of them are recorded in Korea. In this study, we recognized two newly recorded species, *Paraleuctrea* sp. and *Perlomyia* sp from Korea mainly based on the characters of male genitalia. Diagnoses and photographs of the diagnostic characters are provided. Finally, the total number of stonefly species known from Korea is increased to 90. This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR201801201).

Key words: *Paraleuctra*, *Perlomyia*, stoneflies, Korean Peninsula

THE GENUS *PSEUDONEURECLIPSIS* ULMER (PSEUDONEURECLIPSIDAE, TRICHOPTERA) IN JAPAN

S. Inaba[1], T. Nozaki[2]
[1] 3-20, 3-Chome, Shimoda-shi, Shizuoka, 415-0023, Japan
[2] 3-16-15, Midorigaoka Ninomiya-machi, Kanagawa 259-0132, Japan

The genus *Pseudoneureclipsis* Ulmer is a genus composed of 121 species distributed in the Palaearctic and Oriental biogeographic regions, and only five species have been known in Far East Asia: *P. proxima* Martynov, 1934 and *P. ussuriensis* Martynov, 1943 from Russia; *P. botosaneanui* Morse, 2001 from North Korea; *P. tiani* Li, 2001 from China; *P. binael* Malicky, 2014 from Taiwan. Among these five species, latter four species have similar genitalic morphology in male, and are distributed allopatrically. On the other hand, although *P. ussuriensis* and unidentified species have been recorded from Japanese islands, morphological information of them are poorly known.
In this study, we recognize two species, *P. ussuriensis* and a new species, in the Japanese fauna based on examination of extensive specimens collected from Japanese islands. Here, we describe or redescribe adults of these species, and describe immature stages of *P. ussuriensis* for the first time. We also report geographical and individual variations in male genitalia of *P. ussuriensis*. Further study with molecular data may be needed to clarify the relationship between *P. ussuriensis* and allied species.

Key words: *Pseudoneureclipsis ussuriensis*, new species, adults, immature stages, variations

NOTES ON FIVE MICROCADDISFLIES (TRICHOPTERA: HYDROPTILIDAE) RECORDED FOR JAPAN, ONE A NEW DESCRIBED SPECIES

T. Ito[1], N. Shimura[2]
[1] Hokkaido Aquatic Biology, Hakuyo-cho, 3-3-5, Eniwa, Hokkaido, 0616-1434, Japan
[2] Daisan-sanhaimu 106, 2-38-14, Nagatsuta, Midori-ku, Yokohama-shi, Kanagawa, 226-0027, Japan

Notes are provided for five microcaddisflies (Trichoptera, Hydroptilidae) in the Japanese fauna. One is a new species, *Hydroptila nago* Ito, sp. nov., described from southern Japan. A second, *Hydroptila dorsoprocessuata* Botosaneanu, 1993, previously known from South Siberia and the Far East of Russia, is recorded from Japan for the first time and redescribed, and for a third *Hydroptila parapiculata* Yang and Xue, 1994, known from central and southeastern China and central Japan, the male is redescribed. By synonymizing *Ugandatrichia shinshiroensis* Ito et al., 2018, described from central Japan, with a Chinese species, *Allotrichia rhynchophyllum* Zhou et al., 2016, we record the genus *Allotrichia* McLachlan from Japan for the first time. For a fifth species *Stactobia distinguenda* Nozaki and Botosaneanu, 1996, previously known in Japan from the male only, the larva and its case are described.

Key words: *Hydroptila*, *Allotrichia*, *Stactobia*, new species, new record, new synonym, larva, Japan

A MYSTERIOUS REALM OF ANIMALS HIDDEN IN CAVE: AN INTRODUCTION TO THE TROGLOFAUNA

X.K. Jiang[1,2,3], Z.C. Xie[1]
[1] The Key Laboratory of Aquatic Biodiversity and Conservation, Institute of Hydrobiology, Chinese Academy of Sciences, 7 Donghu South Rd., Wuhan 430072, Hubei, China
[2] Institute of Biology, Guizhou Academy of Sciences, 1 Longjiang Lane, Guiyang 550009, Guizhou, China
[3] University of Chinese Academy of Sciences, 19(A) Yuquan Rd., Beijing 100049, China

Caves represent one of the most intriguing ecosystems in the world. Unlike epigean habitats, the subterranean environment completely devoid of sunlight, and usually with high humidity and constant temperature, have produced specialized populations of animals with unique behaviors and characteristics. Based on living habits and morphological characteristics, troglofauna is divided into trogloxenes, troglophiles and troglobites. Troglobites usually be considered as "true cave animal", mostly because of the unique morphological adaptations to subterranean environment, such as unpigmented body, absent or degraded eyes and elongated appendages, and only inhabiting the deep inside of caves. Troglobites were thought to evolve through climatic pressures, such as the Ice Age, or via the "cave refugium" hypothesis. Troglofauna mostly constitute by species of five phyla of animalia, including Arthopoda, Chordata, Mollusca, Annelida and Platyhelminthes. Some cavernicoles show high endemism to a specific cave at the species level, and it is extremely valuable in evolutionary research. However, the close connection to the habitat, makes cave-dwelling animals fragile. Troglofauna is badly in need of investigation and protection. Recently, many expeditions focused on the Chinese troglofauna have been carried out, revealed a mysterious realm of animals hidden in caves. Here, we briefly exhibit the results of these surveys, and introduce some marvelous groups, including aquatic and terrestrial cavernicoles.

Key words: cave, environmental adaptation, troglofauna, taxonomy

THE GENETIC STRUCTURE AND THE MOLECULAR PHYLOGEOGRAPHY OF *EPHEMERA* MAYFLIES

H. Kogawara, M. Takenaka, K. Tojo
Department of Biology, Faculty of Science, Shinshu University, Asahi 3-1-1, Matsumoto, Nagano 390-8621, Japan

River system networks are spatially structured in a hierarchical manner such that habitats are connected linearly with smaller streams progressively flowing into larger streams, and eventually forming larger and larger networks. These networks are highly heterogeneous. Along the length of a river network, habitats transition hierarchically and change drastically from the upstream to downstream areas. The physical attributes of the landscape influence the particular distributional patterns and population structures of species. Firstly, populations of the upstream areas are limited and generally relatively small in size. That is, such populations tend toward miniaturization, and they are usually scattered and isolated with a patchy distribution. As a result, their potential for gene flow between populations is extremely limited, and so there is a higher potential for genetic differentiation between populations, and the influence of random genetic drift is also high. On the other hand, populations of the downstream areas are relatively larger in size. Whereas, populations of the species inhabiting downstream areas are fully inter-connected. As a result, there is the potential for free gene flow between populations, and so their resultant genetic structure is effectively homogeneous. In consideration of this, the mayflies of the genus *Ephemera*, which exhibit the above mentioned typical population structures in river system, is the most interesting group. There are four *Ephemera* mayflies inhabiting the Japanese Islands. Of these, the geographical distribution areas of them overlap widely in Honshu, Shikoku and Kyushu, except for the species, *Ephemera formosana*. When multiple species inhabit the same river system, it is assumed according to various publications that "zonation distribution of habitats" will occur along that riverine environment. In general, it has been considered that *Ephemera japonica*, *Ephemera strigata* and *Ephemera orientalis* accordingly each inhabit the upper, the middle and the lower catchment zones, respectively. As such, *Ephemera* mayflies have been treated as typical, niche partitioned aquatic species, with catchment zone based distribution. Under such circumstances, we conducted genetic analyses of them in order to elucidate the relationship between their population structure and their genetic structure. As results of these analyses, the following things became clear. The scale of gene flow in *E. japonica* was found to be relatively limited. In contrast to this, the scale of gene flow in *E. orientalis* was found to be large. Meanwhile, scale of gene flow in *E strigata* was observed to be intermediate between these two species. We also compared these results with information on other mayfly groups, and we want to discuss the widely accepted hierarchical model of river system networks and their influence on genetic structures, in particular with respect to the strength of connectivity between populations.

Key words: Ephemeroptera, Japanese Island, Phylogeography, zonation distribution

STRUCTURAL CHARACTERISTICS OF CHIRONOMID COMMUNITY AND THEIR INDICATIVE SIGNIFICANCE IN BIOASSESSMENT OF WATER QUALITY IN YONGAN RIVER OF XIANJV, ZHEJIANG

Y.L. Li[1], Q.Q. Kong[1], R.L. Zhang[2], X. Qi[1]
[1] College of Life Science, Taizhou University, Zhejiang, Taizhou 318000, China
[2] College of Fisheries and Life Science, Shanghai Ocean University, Shanghai 201306, China

The structural characteristics of chironomid(Diptera： Chironomidae)community in Yong'an River of Xinajun County, Zhejiang Province, China were studied in August 2016. The result is as follows: 1167 larvae of Chironomidae, in 13 sites of Yong-An River were collected and investigated. 31 chironomid species belonging to 27 genera and 3 subfamilies were identified (Chironominae: 14 genera and 17 species; Orthocladiinae: 9 genera and 10 species; Tanypodinae: 4 genera and 4 species). According to zoogeographic regionalization, 28 species (90.3% of the species in Yong'an River) are both distributed in Palaearctic and Oriental Region, 3 species (9.7% of the species in Yong'an River) are distributed in Oriental Region. *Rheotanytarsus liuae* Wang & Guo, *Conchapelopia* sp., *Polypedilum nubeculosum* (Meigen), *Cricotupus vierriensis* Goetghebuer and *Tanytarsus formosanus* Kieffer are the most abundant. The average density and biomass of chironomidae larvae gradually increased from upstream to downstream of Yongan River, average density 657.8± 473.9ind./m^2 and average biomass 0.51±0.39g/m^2. The distribution and survival of chironomidae larvae are mostly affected by Chlor-a and bottom materials of river. Base on Shannon Index (*H'*), the water quality evaluation of Yong'an River is moderate to heavy polluted, 12 sites are moderate polluted and 1 sites is heavy polluted among 13 sites of Yongan River. Base on Hilsenhoff Index (*BI*), the value is clean to very clean, 4 sites are very clean, 6 sites are clean, 1 sites is normal, and 2 sites are polluted among 13 stream sites of Yong'an River. The results of Shannon Index (*H'*) is different from Hilsenhoff Index (*BI*). The mainly reason may be that Shannon Index (*H'*) is mostly fitter for evaluation of the community of aquatic organism, and the tolerance values of each kind of aquatic organism are dealt as in the same value in Shannon Index (*H'*). The result used by Hilsenhoff Index (*BI*) is more reliable, because Hilsenhoff Index (*BI*) takes account of differences between individuals. Although the results of two index are different, the variation trends are similar.

Key words: Chironominae, species composition, bioassessment of water quality, Yong'an River

DESCRIPTIONS OF FIVE NEW SPECIES OF THE GENUS *HOMOPLECTRA* (TRICHOPTERA, HYDROPSYCHIDAE) FROM JAPAN WITH REASSIGNMENT OF *HOMOPLECTRA TOHOKUENSIS* (KOBAYASHI, 1973)

T. Nozaki
3-16-15, Midorigaoka, Ninomiya-machi, Kanagawa, 259-0132 JAPAN

The genus *Homoplectra* Ross, 1938 was originally described from the western Nearctic region, and 12 species have been reported from the USA. Morphology and biology of immature stages was also provided for some North American species. On the other hand, knowledge of Asian species is quite poor. Only two Chinese species were described based on adults (one from Shaanxi (East Palearctic) and another from Sichuan (Oriental)). No information for immature Asian species is available.
In this study, I describe five new species from Japanese main islands, and transfer *Diplectrona tohokuensis* Kobayashi, 1973 to this genus. Variations in the phallic apparatus are reported for four new species. Descriptions of the immature stage of *H. tohokuensis* and one of the new species are provided. Larvae of these species were found in small seeps and flows in hill or mountain areas. Adult flight season is summer.

Key words: Male, female, immature stages, habitat, new combination

HISTORICAL REVIEW AND AN AMENDED CHECKLIST OF TRICHOPTERA (INSECTA) OF THE KOREAN PENINSULA

S.J. Park, D. Kong
Department of Life Science, Kyonggi University, Suwon 16227, R. O. Korea

Taxonomic studies on adult Trichoptera had been conducted intermittently in the Korean Peninsula until recently. Most studies were accomplished by foreign taxonomists, especially concerning the fauna of the Korean People's Democratic Republic (North Korea) until early 1990s. Since then, several scientists in the Republic of Korea (South Korea) have studied the Trichoptera, but their research was not conducted continuously. Therefore, the knowledge about Trichoptera fauna in Korea is still insufficient and studies on the larval stage are more unsatisfied. The larvae of Trichoptera have been treated as useful indicators for environmental projects such as biological assessment of streams in South Korea since 1980s, but most larvae are not yet identified into species level. A taxonomic checklist for Korean aquatic insects including Trichoptera was published in 2011. However, it overlooked some records of Korean species and taxonomic treatments such as synonymy. National List of Species of Korea by South Korean government, Korean environmental projects, and ecological research on Korean streams use names of Trichoptera from this checklist up to now, therefore a revised checklist of Korean Trichoptera is necessary. In this study, we provide historical review and an amended checklist on Trichoptera for the Korean Peninsula based on bibliographic survey. As a result, 219 species belonging to 69 genera and 24 families are presently known from the Korean Peninsula, of which 35 species are identified as the larval stage. For the further understanding on Korean Trichoptera fauna, steady and continuous research is required.

Key words: Korea, caddisflies, history, catalogue

GLOCHIDIA MORPHOLOGY OF SOME ASIAN MOLLUSCS (BIVALVIA, UNIONIDAE)

E.M. Sayenko
Federal Scientific Center of the East Asia Terrestrial Biodiversity, Far Eastern Branch of Russian Academy of Sciences (FSCEATB FEB RAS), 159 Stoletiya Street, Vladivostok 690022, Russia

The larvae (glochidia) of freshwater bivalves in the family Unionidae are obligate parasites of fishes and amphibians prior to their metamorphosis into juveniles. Morphology of mature glochidia have been used to classify unionids. The purpose of this study is to investigate the glochidial morphology of some Asian unionids. Mature glochidia are taken from (A) formalin-fixed (10%) and (B) ethanol-fixed (75%) molluscs: *Nodularia (=Unio) biwae* Kobelt, 1879 – Biwa L. near Kusatsu City, 08.VI.1982 (A) and near Omihachiman City, Shiga Pref., Honshu Is., Japan, 09.VI.1993 (B); *Lanceolaria grayana* (Lea, 1834) – Gion Creek at Okayama City, Okayama Pref., Honshu Is., Japan, 01.VI.1982 (A) and 03.VI.1993 (B); *Lanceolaria chankensis* Moskv., 1973 – Abramovka R. (Khanka L. basin), 18.IV.1986 (B), Primorye, Russia (B); *Inversiunio yanagawensis* (Kondo, 1982) – Gion Creek at Okayama City, Okayama Pref., Honshu Is., Japan, 13.XI.1993 (A).

Examined species differed in colour of mass of mature glochidia: milky-white in *N. biwae*; from white to light cream in *L. grayana*; light brown in *L. chankensis* and *I. yanagawensis*. Glochidia of all studied species are *Anodonta*-type with hooks. Glochidia of *N. biwae* are the smallest (height 137.5–175 µm, length 145–167.5 µm), and glochidia of *I. yanagawensis* are the largest (height 217.5–240 µm, length 227.5–247.5 µm) among the investigated species. If to compare *Lanceolaria* species, mature glochidia of *L. grayana* (height 192.5–250 µm, length 200–225 µm) are larger than glochidia of *L. chankensis* (height 187.5–192.5 µm, length 197.5–207.5 µm). Glochidia of all investigated species in shape are longer than high, so the height/length ratio of glochidial valves are 0.90–0.97 (*N. biwae*), 0.93–0.98 (*L. grayana*), 0.93–0.95 (*L. chankensis*), 0.93–0.98 (*I. yanagawensis*).

Relative hook height was the largest for *I. yanagawensis* (31–33% of the glochidial valve height) and the smallest for *N. biwae* (only 24–27% of the glochidial valve height). The largest namber of macrospines on the hook (more than 25) were found for *I. yanagawensis* glochidia.

Two main types of microsculpture of the outer surface of glochidial valves were identifed: 1) microgranules varying in size from rough to granular (*L. grayana*, *L. chankensis*) or beaded-globular (*N. biwae*); 2) chaotic loose looped (net) structure (*I. yanagawensis*). Japanese species *N. biwae* differs from *Nodularia* species inhabiting Russian Far East by glochidial microsculpture as *Nodularia* mussels from Russian Far East had glochidia with the only loose looped microsculpture. This fact again raises the question of taxonomic position of *Nodularia biwae*.

Key words: Unionidae, Bivalvia, glochidia, morphology

COMPREHENSIVE DNA BARCODES FOR SPECIES IDENTIFICATION AND DISCOVERY OF CRYPTIC DIVERSITY IN MAYFLY LARVAE FROM SOUTH KOREA

K.I. Suh[1], J.M. Hwang[2], Y.J. Bae[2,3], J.H. Kang[3]
[1] Nakdonggang National Institute of Biological Resources, Gyeongsangbuk-do, 37242, Korea
[2] Korean Entomological Institute, Korea University, Seoul 02842, Korea
[3] Division of Environmental Science and Ecological Engineering, Korea University, Seoul 02842, Korea

DNA barcoding of aquatic macroinvertebrates holds much promise as a tool for taxonomic research and for providing baseline reference for phylogenetic analysis and aquatic ecosystem biomonitoring. It has been known that the mayfly fauna of South Korea includes 77 species (81 in Korean peninsula). We obtained 112 novel sequences of the barcode region of the mitochondrial DNA cytochrome *c* oxidase subunit I gene representing 8 families, 16 genera and 42 species of mayflies (Insecta: Ephemeroptera). No species shared barcode sequences and all can be identified with barcodes with a possible exception of some species. Minimum levels of interspecific genetic distances ranged from 6.7 to 32.9% (mean: 23.7%), whereas average levels of intraspecific divergence was 3.6%. In fact, approximately 28% (15/54) of the species included two or three haplotype clusters showing greater than 5.0% sequence divergence and some values were as high as 32.9%. Many of the species with high intraspecific divergences are para- or polyphyletic and represent the possibility of species complexes. Our study suggests that type or topotype specimens should be sequenced to correctly associate barcode clusters with morphological species concepts and also to determine the status of currently synonymized species.

Key words: DNA barcode, identification, Mayfly, larvae, Korea

PRELIMINARY STUDY ON DIVERSITY OF WHIRLIGIG BEETLES (COLEOPTERA: GYRINIDAE) IN NORTHERN THAILAND

B. Suksai[1], N. Sangpradub[2]
[1] Department of Biology, Faculty of Science, Khon Kaen University, Khon Kaen, Thailand 40002
[2] Applied Taxonomic Research Center, Department of Biology, Faculty of Science, Khon Kaen University, Khon Kaen, Thailand 40002

The objective of this study was to study diversity of adult whirligig beetles in northern Thailand. The diversity of whirligig beetles from 25 sites in Chiang Mai, Chiang Rai, Lampang, Mae Hong Son, Nan, Phayao, Phrae and Uttaradit Provinces of northern Thailand were investigated during the year 2017 to 2018. Samples were collected by using a D-frame dip net with 450 µm mesh size from streams, creeks, lakes and rivers. As a result, a total of 1,879 individuals of whirligig beetles belonging to four genera were classified: *Patrus* (99.67%), *Orectochilus* (4.63%), *Porrorhynchus* (1.38%) and *Gyrinus* (0.32%). *Patrus* was the most abundant and the highest diversity (13 morphospecies) whirligig beetles found in this study. The identification of whirligig beetles to the species level is ongoing.

Key words: diversity, Whirligig beetles, Northern Thailand

AN UPDATE TO THE TRICHOPTERA FAUNA OF SOUTH KOREA WITH A REPORT OF NEW RECORD

J.C. Uy Christine[1], N. Sareein[2], V.C. Duong[2], Y.J. Bae[1,2]
[1] Department of Life Sciences, Graduate School, Korea University, Seoul, Korea
[2] Department of Environmental Science and Ecological Engineering, Graduate School, Korea University, Seoul, Korea

A total of 164 species of Trichoptera have been recorded from South Korea. Species from the family Rhyacophilidae is the most abundant with 29 species, followed by Limnephilidae with 20 species, and Leptoceridae with 19 species. One species *Ceraclea indistincta* Forsslund, 1935 (Leptoceridae) which is distributed in China and Russia were reported for the first time in South Korea. The newly recorded species was redescribed and redrawn. This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR201801201).

Key words: Trichoptera, South Korea, new record, *Ceraclea indistincta*

A REDESCRIPTION OF *CHIRONOMUS* (*CHIRONOMUS*) *FLAVIPLUMUS* TOKUNAGA (DIPTERA: CHIRONOMIDAE) FROM CHINA

R.L. Zhang[1,2,3], D. Zhou[1,2,3], S. Chen[1,2,3]
[1.] Centre for Research on Environmental Ecology and Fish Nutrion (CREEFN) of the Ministry of Agriculture, Shanghai Ocean University, Shanghai 201306, China
[2.] Key Laboratory of Exploration and Utilization of Aquatic Genetic Resources (Shanghai Ocean University), Ministry of Education, Shanghai 201306, China
[3.] National Demonstration Center for Experimental Fisheries Science Education (Shanghai Ocean University) , Shanghai 201306, China

Based on the material cultured in the lab, the egg, larva, pupa and imago of *Chironomus* (*Chironomus*) *flaviplumus* Tokunaga are described and diagnosed. Illustrations of all stages as well as a partial COI gene sequence are presented.

Key words: Chironomidae, *Chironomus flaviplumus*, redescription, all stages, COI

BIODIVERSITY AND DISTRIBUTION OF EPHEMEROPTERA, PLECOPTERA AND TRICHOPTERA ALONG LONGITUDINAL ZONES OF THE KHE STREAM, QUANG NAM PROVINCE, VIETNAM

V.C. Duong[1], X.N. Ngo[2], V.V. Nguyen[3], Y.J. Bae[1]
[1] Department of Environmental Science and Ecological Engineering, Korea University, Seoul, Korea
[2] Institute of Ecology and Works Protection, 267 Chua Boc, Dong Da, Hanoi, Vietnam
[3] Faculty of Biology, VNU University of Science, 334 Nguyen Trai, Thanh Xuan, Hanoi, Vietnam

A field study was implemented to evaluate the longitudinal change of taxonomic diversity and functional feeding groups (FFGs) distribution of Ephemeroptera, Plecoptera and Trichoptera (EPT) in Khe The stream, Quang Nam province, Vietnam. During the period 2016-2017, thirty studied sites were investigated along the stream, including Zone 1 (headwaters), Zone 2 (transfer zone) and Zone 3 (depositional zone). Mayflies, stoneflies, and caddisflies were recorded at all zones with a total of 82 species belonging to 60 genera and 26 families. The diversity indices (Shannon-Weiner and Margalef) of EPT were highest at Zone 1, followed by Zone 2 and lowest at Zone 3. The result of ANOSIM analysis showed that there was a significant difference of species composition among three zones. To assess the longitudinal distribution of these organism based on functional feeding groups, the EPT assemblages were also classified into five groups: collector-gatherers (CG), collector-filterers (CF), shredders (SH), scrappers (SC) and predators (P). In this study, CG was the predominant group inhabiting all three reaches. SC group decreased from Zone 1 to Zone 3 while CF group increased from Zone 3 to Zone 1. SH and P groups accounted for a modest steady number among three zones. The result illustrated that Khe The stream was suitable for CG group.

Key words: biodiversity, distribution, EPT, functional feeding group, Quang Nam province, Vietnam.

DIVERSITY OF TASTE PREFERENCES IN BENTHIVOROUS CARP FISHES

O.M. Isaeva[1], A.O. Kasumyan[2]
[1] Kamchatka State Technical University, Department of Water Bioresources and Aquaculture, Vilyuiskaya st. 56, Petropavlovsk-Kamchatsky, 638000 Russia, 638000
[2] Moscow State University, Faculty of Biology; Leninskie Gory, Moscow, 119992 Russia 119899

Carp fishes (Cyprinidae) are most common and numerous fish species in freshwaters of the Nothern Hemisphere. Many of them are benthiorous and play significant role in freshwater ecosystems. The relationships between carp fishes and benthic invertebrate preys are based on selective feeding of fish. Fish use distant senses as vision, olfaction and lateral line for the preliminary evaluation of encountered prey but use taste system for final decision to swallow or refuse grasped prey. Only prey with appropriate taste properties will be consumed by fish. The main goal of present study was to evaluate and to compare the taste preferences in benthivorous carp fishes common in boreal area of Eurasia – common carp *Cyprinus carpio*, bream *Abramis brama*, roach *Rutilus rutilus*, tench *Tinca tinca*, bitterling *Rhodeus sericeus amarus*, goldfish *Carassiua auratus gibelio*, crucian carp *Carassius carassius*.

It was found that carp fishes have different taste preferences for 4 classical taste substances and 21 free L-amino acids used as taste stimuli. As example, citric acid is highly palatable for common carp, tench and bream but has aversive taste for all other fishes. Cysteine is most palatable amino acid for common carp and tench but is deterrent substance for bitterling and crucian carp and indifferent taste stimuli for gold fish, bream and roach. Between 21 free amino acids tested 12 were palatable for tench, 9 for roach and gold fish and only 6 and 4 for common carp and bitterling. No one amino acids were palatable for crucian carp. Significant correlation were not found in pair-wise statistical comparison between all 7 fishes studied ($p > 0.05$). High species specificity of taste spectra in closely related fishes inhabit the same waters depresses interspecies feeding competition and leads to increasing diversity of feeding relationships links between benthivorous fishes and benthic invertebrate animals. The study was supported by the Russian Foundation for Basic Research (project 16-04-00322).

Key words: carp fishes, taste preferences, benthos, water ecosystems

TRICHOPTERA TAXONOMY AND FAUNA OF DABIE MOUNTAINS

S. Qiu, Y.J. Yan
Huazhong University of Science and Technology, #1037 Luo-yu Road, Wuhan, Hubei, P. R. China

Trichoptera, also called caddisflies on adult stage, are completely aquatic at larva stage and have a preference for clean, cold freshwater bodies. Because many species are very sensitive to pollutants and other disturbances, they can be used as bio-monitoring indicators for various aquatic ecosystems. In this study, we took 27 samplings at 17 sites in Dabie Mountains, east central China, during 2014 to 2015. A total of 8279 Trichoptera specimens were collected. Identification indicated that in this study, we collected a total of 130 species of 50 genera, with 106 known species, and 24 new species or suspected new species. By checking the references, we also found 11 more species that are recorded in Dabie Mountains which we did not collected.

At the same time, we also analyzed the biogeographical distribution of Trichoptera in Dabie Mountains. The results showed that Most species collected in Dabie Mountains only distribute in east central China close to Qinling-Huaihe line; only a little species are distribute in south or southwest. Considering World Biogeographical Regions, 56 species are distributed in Oriental Region, 48 species are endemic to Dabie Mountains, and 34 species of Oriental-Palearctic Region, constituting the main body of the fauna of Trichoptera in Dabie Mountains. From the results, we can conclude that there is a closer connection between the Trichoptera fauna of Dabie Mountains and humid region, relatively, the connection between arid region is much weaker.

Key words: Caddisfly, Dabie Mountains, fauna, taxonomy

SCALE EFFECTS ON ELEVATIONAL PATTERNS OF TAXONOMIC RICHNESS AND FUNCTIONAL DIVERSITY OF AQUATIC INSECTS IN THE UPPER LANCANG-MEKONG BASIN

H.Y. Wei[1], K. Chen[1], B.X. Wang[1], N. Ding[1], Q.W. Chen[2]
[1] Department of Entomology, Nanjing Agricultural University, Nanjing, Jiangsu 210095 P.R. China
[2] Center for Eco-environmental Sciences Research, Nanjing Hydraulic Research Institute, Nanjing, Jiangsu 210024 P. R. China

Scale dependent species and functional diversity of aquatic insects remain unexplored in the context of strong elevational gradient. We aimed to evaluate effect of spatial extent on large-scale elevational patterns in taxon richness and functional diversity of aquatic insects in streams across three climatic zones. We sampled data at 120 stream sites from the upper Lancang-Mekong river across frigid, sub-tropical, and tropical climates along an elevational gradient of 500-4,500 m a.s.l. We analyzed patterns in species richness (SR) and Functional Richness (FRic), Functional Evenness (FEve) and Functional Divergence (FDiv) along elevation at two spatial scales: the local scale (at each site) and regional scale (along 100-m elevational bands). Only FRic decreased monotonically with elevation at local scale. However, SR and FRic decreased while FDiv showed a unimodal pattern with elevation at regional scale. Our results showed that species and functional diversity of aquatic insects could respond in fundamentally different ways to elevational gradient at different spatial scales.

Key words: biodiversity, traits, China, macroecology

Authors index

* As Oral and/or Poster presentation presenter

BAE Y.J. yjbae@korea.ac.kr
Session 02: P12
Session 03: P16
Session 04: P30, 72 & 74
Session 05: P37, 44, 45 & 76

BAZHINA L.V. librlil@mail.ru
Session 02: P55*

CAI Y.J. caiyj@niglas.ac.cn
Session 01: P51*
Session 03: P20

CHEN K. kai.chen@njau.edu.cn
Session 01: P1*, 53 & 54
Session 03: P14, 15 & 17
Session 04: P61
Session 05: P38, 41 & 79

CHON T.S. tschon.chon@gmail.com
Session 05: P35*

CUI Y.D. ydcui@ihb.ac.cn
Session 01: P8
Session 02: P9 & 13
Session 04: P25* & 33

DING N. dingningyx@gmail.com
Session 03: P14*
Session 05: P38 & 79

DU Y. duyingiwhr@163.com
Session 05: P36*

DUONG V.C. yjbae2025@naver.com
Session 04: P74
Session 05: P37* & 76*

FU R. 1223629072@qq.com
Session 04: P61*
Session 05: P46

GAO J. 2016102085@njau.edu.cn
Session 01: P52 & 53
Session 03: P15*
Session 05: P41 & 46

HAN N. nahan4559njnu@163.com
Session 04: P23 & 32

HAN X.M. hanxuemei916@163.com
Session 03: P59*

HE S.W. siwenhe0909@gmail.com
Session 01: P54
Session 03: P17
Session 05: P38*

HE Y.J. hyjjayel@163.com
Session 02: P9*

HU Y.L. 2016102086@njau.edu.cn
Session 04: P62*
Session 05: P41

HWANG J.M. msmay74@gmail.com
Session 04: P63* & 72
Session 05: P45

INABA S. inabashu3@yahoo.co.jp
Session 04: P64*

ISAEVA O.M. olisa24@bk.ru
Session 05: P77*

ITO T. tobikera@siren.ocn.ne.jp
Session 04: P65*

JAITRONG B. nebneb1122@gmail.com
Session 01: P5
Session 02: P10*

JIANG X.K. antoma@126.com
Session 04: P66*

KANG J.H. jihyounkang@korea.ac.kr
Session 02: P12
Session 04: P30, 63 & 72*

KONG Q.Q. kongqianqian0605@outlook.com
Session 04: P21*, 68

LI B. binglee527@gmail.com
Session 01: P2*

LI Z.F. 1282582837@qq.com
Session 05: P39* & 42

LIN C.L. linchenlu0939@163.com
Session 02: P58*

LIN K.X. linkuixuan@aliyun.com
Session 01: P3*

LIN X.L. lin880224@gmail.com
Session 04: P21 & 22*

LIU Y.D. liuyuedan@scies.org
Session 01: P4*

LIU Y.L. liuyl1026@126.com
Session 01: P3

LIU Z.Y. 1605220162@qq.com
Session 05: P40*

LU H.M. hmlu@nhri.cn
Session 02: P11*

MA Z.X. 952718141@qq.com
Session 04: P23* & 32

MBAO E. 2017202060@njau.edu.cn
Session 03: P17
Session 05: P41*

MENG X.L. xingliang01@ihb.ac.cn
Session 05: P39 & 42*

NGO X.N. ngoxuannam@hus.edu.vn
Session 02: P56*
Session 05: P76

NGUYEN V.V. vinhnv@hus.edu.vn
Session 02: P56
Session 05: P37 & 76

NIKULINA T.V. nikulinatv@mail.ru
Session 02: P57*
Session 05: P43*

NOZAKI T. takao.nozaki@nifty.com
Session 04: P64 & 69*

PARK S.H. yjbae2025@naver.com
Session 03: P16*
Session 05: P45
PARK S.J. sjp7427@gmail.com
Session 04: P70*
PELINGEN A.L.
arthien.pelingen@obf.ateneo.edu
Session 04: P24*
PENG L. 1030528830@qq.com
Session 04: P62
PENG Y. pydaisy@163.com
Session 04: P25 & 33
PHALARAKSH C. chitcholp@gmail.com
Session 01: P7
Session 02: P12
Session 05: P44
PHOSANGA K. narirynariry@gmail.com
Session 01: P5*
Session 02: P10
QI X. qixin0612@tzc.edu.cn
Session 04: P21 & 68*
QIU S. shirleyqiu@aliyun.com
Session 05: P78*
RAHONG P. panida.mooh@gmail.com
Session 05: P44*
RAJPER A.R. razarajper6@gmail.com
Session 03: P15 & 17*
Session 05: P38
SAREEIN N. yjbae2025@naver.com
Session 02: P12*
Session 04: P74
Session 05: P37 & 44
SAYENKO E.M. sayenko@biosoil.ru
Session 04: P26* & 71*
SEOK S.W. yjbae2025@naver.com
Session 03: P16
Session 04: P63
Session 05: P45*
SUHAILA A.H. ahsuhaila@usm.my
Session 01: P6*
SUKSAI B. ben_kku@hotmail.co.th
Session 04: P73*
SUN C.H. chsun@njau.edu.cn
Session 04: P62
SUZUKI T. suzuki_t@shinshu-u.ac.jp
Session 04: P27*
TAKENAKA M. 16st404a@shinshu-u.ac.jp
Session 04: P28*,67
TAN C.Z. 2017102084@njau.edu.cn
Session 01: P53
Session 05: P46*
TECHAKIJVEJ C. chotiwutte@gmail.com
Session 01: P7*
Session 05: P44
TOJO K. ktojo@shinshu-u.ac.jp
Session 04: P27, 28, 31 & P67*
TONG X.L. xtong@scau.edu.cn
Session 04: P29*
UY CHRISTINE J.C. yjbae2025@naver.com
Session 04: P30* & 74*
WANG B.X. wangbeixin@njau.edu.cn
Session 01: P1, 52, 53 & 54
Session 02: P11
Session 03: P14, 15 & 17
Session 04: P61 & 62
Session 05: P38, 41, 46 & 79
WANG H.L. 295174334@qq.com
Session 03: P60*
WANG J. yuzhoumanyou@163.com
Session 05: P39 & 42
WANG L. Wangl709@nenu.edu.cn
Session 02: P58
Session 03: P18*
WANG X.H. xhwang@nankai.edu.cn
Session 04: P21 & 22
WANG Y. 15895982833@163.com
Session 01: P52*
Session 04: P62
Session 05: P41
WEI H.Y. 2017102083@njau.edu.cn
Session 05: P79*
WU C. 1031645568@qq.com
Session 01: P53*
Session 05: P41 & 46
WU D.Y. dayongwu@hotmail.com
Session 05: P34*
WU J.Y. wujunyan0000@163.com
Session 01: P8*
XIANG H.Y. hongyong.xiang@xjtlu.edu.cn
Session 03: P19*
XIE Z.C. zhcxie@ihb.ac.cn
Session 04: P66
Session 05: P39, 42 & 47
XING Y. may1927@163.com
Session 05: P47*
YANG X.M. 923404683@qq.com
Session 03: P59
YANO K. 18hs406b@shinshu-u.ac.jp
Session 04: P31*
YAO K.S. yks318517@163.com
Session 02: P13*
YU Y. yuyangle@126.com
Session 05: P48*
ZHANG H.P. zhang2success@126.com
Session 05: P48
ZHANG J.W. 2016202021@njau.edu.cn
Session 01: P54*
Session 03: P17
ZHANG R.L. rlzhang@shou.edu.cn
Session 04: P68 & 75*

ZHANG W. zyhnjnu@163.com
Session 04: P23 & 32*
ZHANG Y.X. yixin.zhang@xjtlu.edu.cn
Session 03: P19
ZHANG Y. yzhang@niglas.ac.cn
Session 03: P20*
ZHOU C.F. zhouchangfa@njnu.edu.cn
Session 04: P23 & 32
ZHOU T.T. ttzhou319@163.com
Session 04: P33*

ATKINSON D. Session 03: P19
BAEK M.J. Session 05: P45
BERG M.P. Session 03: P14
CHEN G. Session 02: P58
CHEN L.M. Session 02: P11
CHEN Q.W. Session 05: P79
CHEN S. Session 04: P75
CHEN X.L Session 01: P4
CHENG L. Session 03: P20
CHENG X. Session 05: P34
COOPER K.M. Session 05: P42
CORNELISSEN J.H.C. Session 03: P14
DENG J.M. Session 01: P51
FREITAG H. Session 04: P24
GAO Y.Z. Session 03: P18
GIESY J.P. Session 01: P4
GONG Y.W. Session 02: P58
GONG Z.J. Session 01: P51
GUO S.J. Session 03: P59
HEINO J. Session 01: P51
Session 03: P20
Session 05: P39
HU Z.X. Session 01: P51
HUGHES R.M. Session 01: P1
JANG Y.H. Session 05: P35
JIANG X.M. Session 05: P39 & 42
JITMANEE C. Session 01: P5
Session 02: P10
JUNG N. Session 05: P35
KASUMYAN A.O. Session 05: P77
KIM J.S. Session 05: P37
KIM W.G. Session 05: P37
KLEUSH V.O. Session 02: P55
KOGAWARA H. Session 04: P67
KONG D. Session 04: P70
KWAK G. Session 05: P35
LEEM J.B. Session 05: P35
LI H.T. Session 03: P60
LI K.Y. Session 03: P20
LI L. Session 01: P3
LI N. Session 03: P60
LI X.H. Session 02: P11
LI Y.L. Session 04: P21 & 68
LI Y.Y. Session 03: P59
LIU L.S. Session 01: P3
LIU Y.W. Session 02: P58
LIU Z.Y. Session 01: P4
MOHD FAKHRULLAH SALAFUSALAM M.A.
Session 01: P6
MURANYI D. Session 04: P63
NGUYEN N.H. Session 02: P56
OLSON J.R. Session 01: P1
OMONDI S. Session 05: P41
PARK S.W. Session 04: P63
PENG Z.H. Session 01: P8
QIN B.Q. Session 01: P51
QU X.D. Session 05: P36 & 48
RAJU S. Session 03: P19
SANGPRADUB N. Session 04: P73
SEMENCHENKO K.A. Session 02: P55
SHI W.F. Session 04: P29
SHIMURA N. Session 04: P65
SHU F.Y. Session 02: P9
SHU S. Session 03: P60
SITOKI L. Session 05: P41
SOROKA M. Session 04: P26
SUH K.I. Session 04: P72
SUN R.H. Session 05: P34
TAN Y. Session 02: P58
TAO M. Session 03: P60
WANG H Session 01: P4
WANG H.J. Session 02: P9
WANG H.Z. Session 01: P8
Session 02: P9
WANG Q. Session 03: P60
WANG X.L. Session 01: P51
Session 03: P20
WU F.C. Session 01: P4
WU J.B. Session 02: P11
XU J. Session 01: P53
XU X. Session 03: P60
YAN Y.J. Session 05: P78
YANG G.F. Session 05: P36
YANG H.J. Session 02: P58
Session 03: P18
YIN H.B. Session 01: P51
YIN S.L. Session 01: P53
YOON T.J. Session 02: P12
ZHANG H.W. Session 03: P60
ZHANG L. Session 03: P20
ZHANG M. Session 05: P36 & 48
ZHANG Q.H. Session 03: P60
ZHANG Y. Session 01: P51
ZHANG Y.H. Session 05: P36
ZHOU D. Session 04: P75
ZHU X. Session 05: P36