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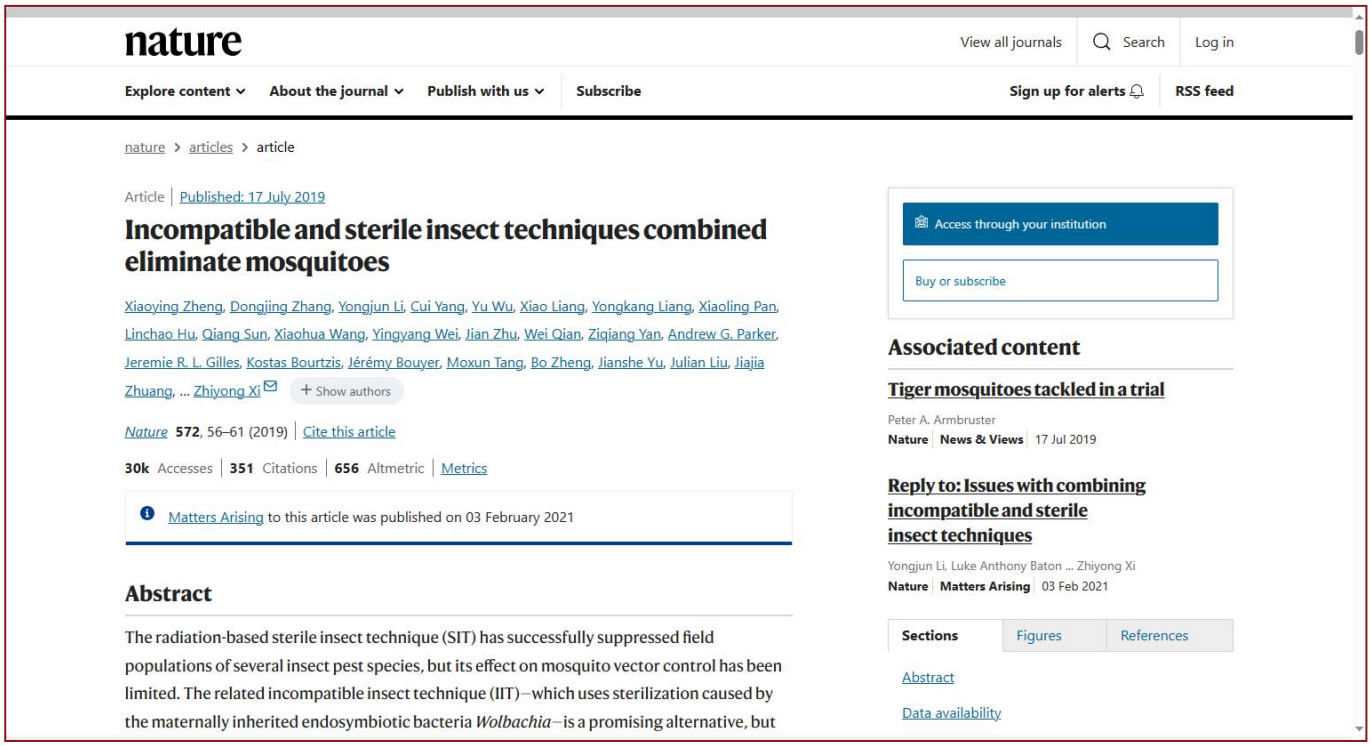

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Article | Published: 17 July 2019

Incompatible and sterile insect techniques combined eliminate mosquitoes

Xiaoying Zheng, Dongjing Zhang, Yongjun Li, Cui Yang, Yu Wu, Xiao Liang, Yongkang Liang, Xiaoling Pan, Linchao Hu, Qiang Sun, Xiaohua Wang, Yingyang Wei, Jian Zhu, Wei Qian, Ziqiang Yan, Andrew G. Parker, Jeremie R. L. Gilles, Kostas Bourtzis, Jérémy Bouyer, Moxun Tang, Bo Zheng, Jianshe Yu, Julian Liu, Jiajia Zhuang, ... Zhiyong Xi + Show authors

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Matters Arising to this article was published on 03 February 2021

Abstract

The radiation-based sterile insect technique (SIT) has successfully suppressed field populations of several insect pest species, but its effect on mosquito vector control has been limited. The related incompatible insect technique (IIT)—which uses sterilization caused by the maternally inherited endosymbiotic bacteria *Wolbachia*—is a promising alternative, but

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Yongjun Li, Luke Anthony Baton ... Zhiyong Xi
Nature | **Matters Arising** | 03 Feb 2021

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Abstract

Data availability

If *w*Pip-positive larvae were observed, the sample was further screened by standard PCR using primers specific to the *ribosomal protein S6* (*rps6*) gene of *C. quinquefasciatus*, the only possible mosquito species with *w*Pip co-occurring in the field sites, to exclude any false positives resulting from the collection of *Culex* larvae in the ovitraps. The specific-primers used for the assay were designed for *rps6* gene and consisted of: *rps6F*: 5′-TGCCGCGTCGTCTTGAATC-3′; and *rps6R*: 5′-GTATTGACCTCGTCGCGCTT-3′. The 20 μl PCR reaction consisted of 2 μl DNA template, 10 μl PCR Master Mix (Dongsheng), 1 μl of each primer (10 μM) and 6 μl ddH_2O. The PCR conditions comprised of 5 min at 98 °C, followed by 40 cycles of 30 s at 98 °C, 5 s at 55 °C, 30 s at 72 °C, and then 10 min at 72 °C for the final extension. PCR products were electrophoresed on a 1.5% agarose gel, which contained 1 μg/ml ethidium bromide. If a product size of approximately 350 bp was obtained, the sample was considered to contain *w*Pip derived from *Culex* mosquitoes.

Incompatible and sterile insect techniques combined eliminate mosquitoes.
Nature. (IF: 69.50)

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Current Biology

Volume 31, Issue 23, 6 December 2021, Pages 5314-5326.e10

Article

Narrow mutational signatures drive acquisition of multidrug resistance in the fungal pathogen *Candida glabrata*

Ewa Ksiezopolska[1,2,5], Miquel Àngel Schikora-Tamarit[1,2,5], Reinhard Beyer[3], Juan Carlos Nunez-Rodriguez[1,2], Christoph Schüller[3], Toni Gabaldón[1,2,4,6,7]

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Referred to by Antifungal drug resistance: Deciphering the mechanisms governing multidrug resistance in the fungal pathogen *Candida glabrata*
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Target *FKS* and *ERG3* sequencing

All ani-exposed samples (ANI, ANIFLZ and FinA) were examined for mutations in one region of *FKS1* and two regions of *FKS2* encompassing echinocandin resistance mutational HSs.[5] Three samples without mutations in the above-mentioned HSs were also inspected in the HS2 of *FKS1*. All the new *FKS* mutations are in Data S2. We used PCR primers described earlier[58] (Table S5). ANI samples not subjected to WGS were also amplified by two PCRs with two sets of primers (Table S5) to obtain *ERG3* sequences. PCRs were carried out by using Taq DNA polymerase from DongShengBio. The reaction mixture included primers of concentration of 0.4 μM, 20 μL Taq DNA polymerase, 1 μL liquid sample grown for 24-48 h in YPD and water up to a final volume of 40 μL. Optimase ProtocolWriter was used to develop conditions for each primer set.

We tested for the possible trajectories of final *FKS* and *ERG3* mutations in the 10 ANI samples subjected to WGS and presenting *ERG3* alterations to infer which might have appeared first in the evolution. We selected and analyzed single colonies from our glycerols stocks of stored populations after the 2nd passage at 0.032, 0.064, 0.128 and 0.256 ug/ml ani (beginning of the adaptation). PCRs were carried out as described above.

Narrow mutational signatures drive acquisition of multidrug resistance in the fungal pathogen Candida Glabrata.
Current Biology. (IF: 10.90)

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Marine Pollution Bulletin
Volume 184, November 2022, 114112

Seasonal variation, virulence gene and antibiotic resistance of *Vibrio* in a semi-enclosed bay with mariculture (Dongshan Bay, Southern China)

Qiancheng Gao [a], Xiaowan Ma [c 1], Zhichao Wang [b], Haisheng Chen [d], Yu Luo [b], Bi Wu [a], Shanni Qi [a], Miaozhen Lin [a], Jing Tian [a], Ying Qiao [c], Hans-Peter Grossart [e f], Wei Xu [b c], Lixing Huang [a]

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Abstract

In this study, the virulence genes, antibiotic resistance of culturable Vibrio and the environmental factors affecting *Vibrio* abundance were analyzed in four seasons in

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2.3. Detection of virulence genes

Nine virulence genes (*vvhA*, *luxR*, *tdh*, *trh*, *toxR*$_{vc}$, *flaC*, *ChiA*, *hlyA* and *vhpA*) of *Vibrio* species were amplified by PCR. The primers are given in Table 1. The final volume of the amplification PCR was 50 μL, including 2 μL DNA template, 25 μL 2 × pfu Mix (Guangzhou Dongsheng Biotech, Guangzhou, China), 2 μL forward and reverse primers, and 19 μL ddH_2O. PCR products were separated on a 2 % agarose gel by using 145 V/360 A, and the bands were recorded by an image analyzer BioDoc-It™ system (UVP Inc., Upland, CA, USA).

Seasonal variation, virulence gene and antibiotic resistance of Vibrio in a semi-enclosed bay with mariculture (Dongshan Bay, Southern China). Marine Pollution Bulletin. (IF: 7.00)

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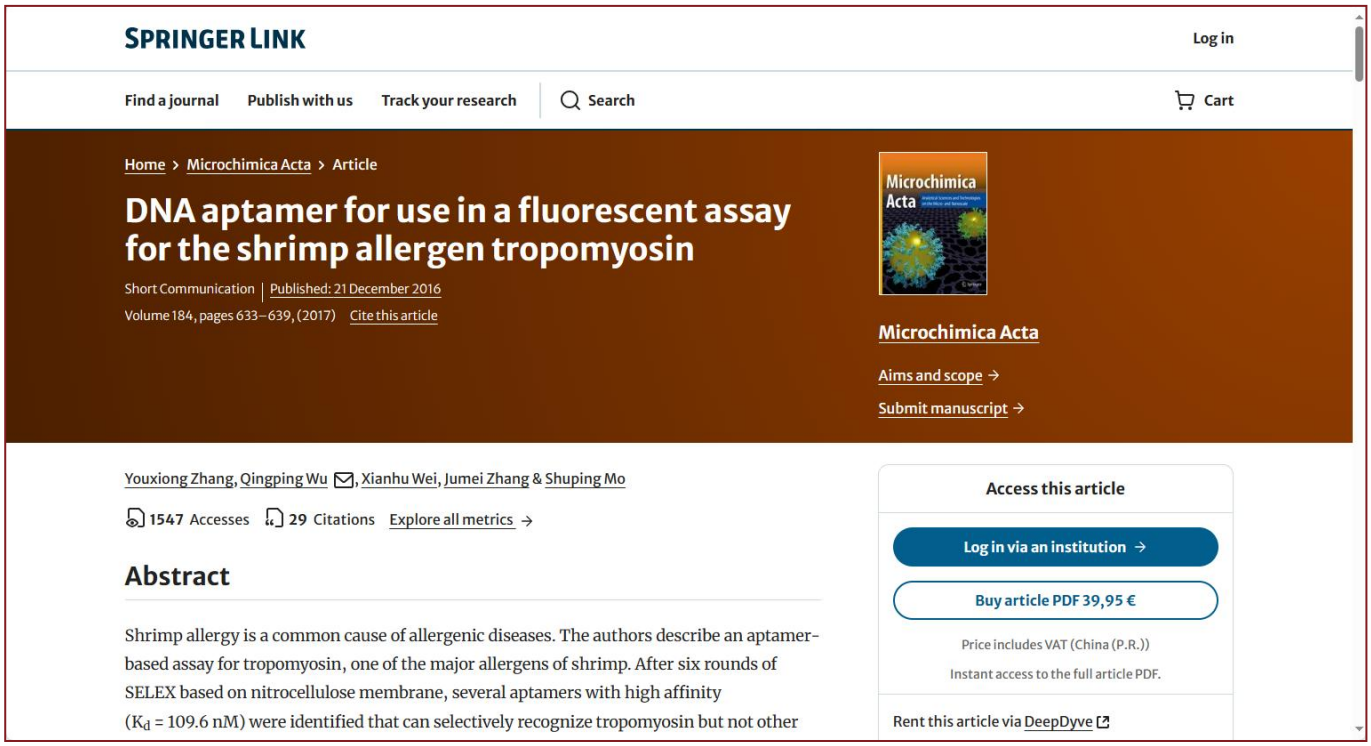

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DNA aptamer for use in a fluorescent assay for the shrimp allergen tropomyosin

Short Communication | Published: 21 December 2016

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Abstract

Shrimp allergy is a common cause of allergenic diseases. The authors describe an aptamer-based assay for tropomyosin, one of the major allergens of shrimp. After six rounds of SELEX based on nitrocellulose membrane, several aptamers with high affinity (K_d = 109.6 nM) were identified that can selectively recognize tropomyosin but not other

the progression of SELEX, the amount of eluted ssDNA was measured by Nanodrop device (Thermo-Scientific, USA). An ssDNA library for the following round was prepared by an asymmetric PCR protocol using HS™ Mix (Dongsheng Biotech, Guangzhou, China, http://www.dongshengbio.com) with a molar ratio of primer-Fw/primer-Rv = 50:1. All the PCR amplifications were performed as follows: 1 cycle at 95 °C for 5 min; 30 cycles at 94 °C for 40 s, 50 °C for 30 s, 72 °C for 30 s; followed by 1 cycle at 72 °C for 10 min. The screening was repeated six times, and the last round eluted ssDNAs were amplified by standard PCR protocol. The

DNA aptamer for use in a fluorescent assay for the shrimp allergen tropomyosin. Microchimica Acta. (IF: 6.41)

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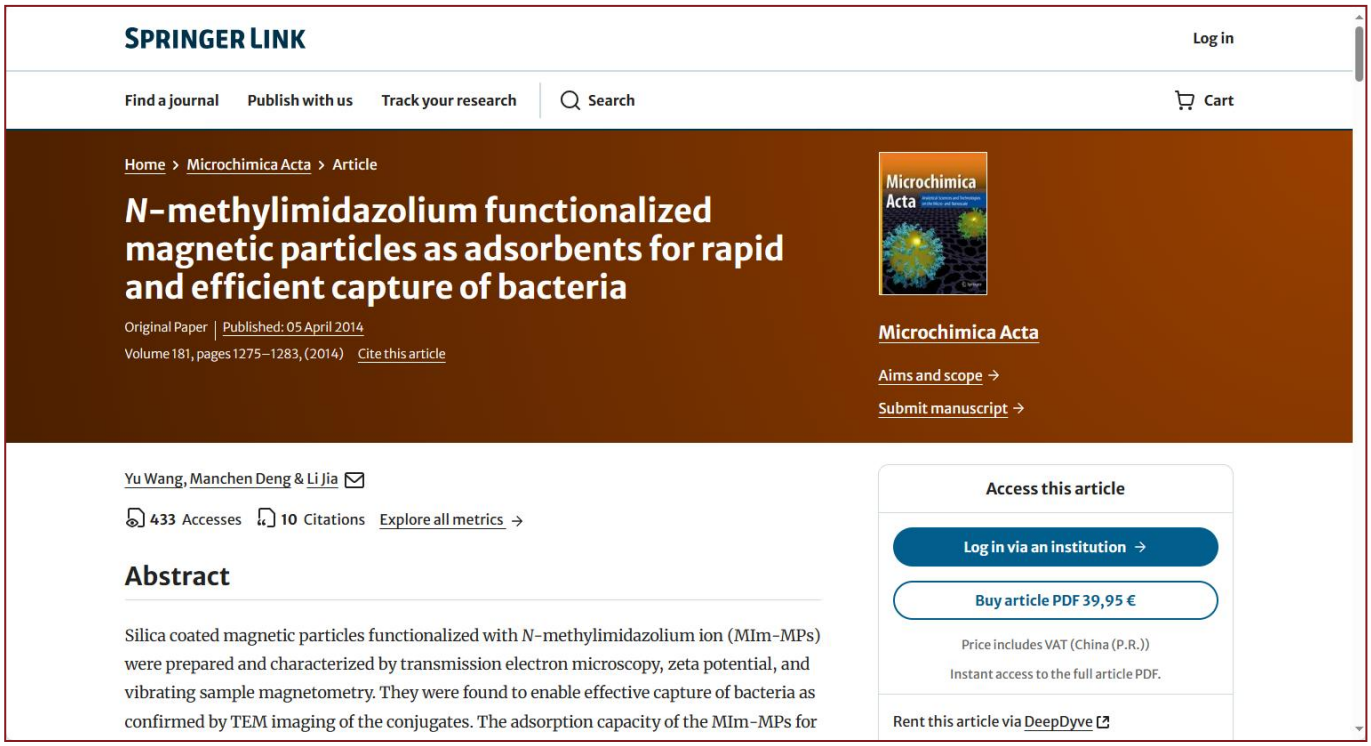
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N-methylimidazolium functionalized magnetic particles as adsorbents for rapid and efficient capture of bacteria

Original Paper | Published: 05 April 2014

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Abstract

Silica coated magnetic particles functionalized with *N*-methylimidazolium ion (MIm-MPs) were prepared and characterized by transmission electron microscopy, zeta potential, and vibrating sample magnetometry. They were found to enable effective capture of bacteria as confirmed by TEM imaging of the conjugates. The adsorption capacity of the MIm-MPs for

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A GeneRuler 100-bp DNA ladder was purchased from Fermentas (Beijing, China, www.fermentas.com) and consisted of ten fragments ranging from 100 to 1,000 bp with a total concentration of 0.5 mg mL^{-1}. Taq DNA polymerase (5 U μL^{-1}) was purchased from Dongsheng Biotech (Guangzhou, China, www.dongshengbio.com). 25 mM $MgCl_2$, 10×PCR buffer (100 mM Tris–HCl [pH 8.3], 500 mM KCl), and deoxynucleotide triphosphate (dNTP) mixture (including dATP, dGTP, dCTP, and dTTP, where the concentration of each dNTP was 2.5 mM) were purchased

N-methylimidazolium functionalized magnetic particles as adsorbents for rapid and efficient capture of bacteria. Microchimica Acta. (IF: 6.41)

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Volume 527, 15 October 2020, 735495

Screening and characterization of sex-specific markers developed by a simple NGS method in mandarin fish (*Siniperca chuatsi*)

Chong Han [a b], Qiaoying Zhu [a b], Haoming Lu [a], Chongwei Wang [a], Xingni Zhou [a], Cheng Peng [c], Lin Tang [a], Linqiang Han [d], Jiehu Chen [e], Shuisheng Li [a], Guifeng Li [a], Haoran Lin [a b], Yong Zhang [a b]

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Abstract

Sex-specific markers are the prerequisite for interpreting the mechanisms of sex determination and sex control breeding in fish. Here, we provided a simple next generation sequencing strategy to identify potential sex-specific sequences in mandarin fish (Siniperca chuatsi) that is a greatly important freshwater fish in China. Through

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volume of 10ul, including 5ul 2xTaqMasterMix (DSBIO, China), 0.5ul each specific primer (10uM), 0.5ul DNA template and 3.5ul ddH_2O. The PCR amplification reaction was carried out as following: pre-denaturation at 95 °C for 5 min; followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 58 °C for 30 s, and extension at 72 °C for 30s; and finally an extension step of 72 °C for 5 min. The amplified products were separated by 1.5% agarose gel. Then, another 16 DNAs (8 females

Screening and characterization of sex-specific markers developed by a simple NGS method in mandarin fish (Siniperca chuatsi).
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Aquaculture
Volume 562, 15 January 2023, 738833

Screening and characterization of X chromosome-specific markers in mandarin fish (*Siniperca chuatsi*)

Shiyan Liu [a, b], Chong Han [a], Jingjun Huang [a, c], Qiaoying Zhu [a], Dingrui Liu [a], Linqiang Han [c], Shuisheng Li [a], Guifeng Li [a], Haoran Lin [a, b], Yong Zhang [a, b]

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Abstract

The mandarin fish (Siniperca chuatsi) is an important aquaculture fish. All-male mandarin fish culture has the advantages of higher profits, more uniform size and lower energy consumption of gonadal development. However, the lack of accurate sex-specific markers has hampered the all-male breeding of this species. Herein, we successfully adopted a next generation sequencing strategy to identify potential X chromosome-

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Based on the filtrated X chromosome-specific sequences, primers were designed by Primer Premier 5.0 software (http://www.premierbiosoft.com/). DNAs from XX, XY and YY individuals were used as templates to test the feasibility and universality of X chromosome-specific markers. Each PCR reaction was performed in a total volume of 10 μl, including 5 μl 2 × Tap MasterMix (DSBIO, China), 0.5 μl each specific primer, 0.5 μl DNA template and 3.5 μl ddH_2O. The PCR amplification reaction was carried out as following: pre-denaturation at 95 °C for 5 min; followed by 30 cycles of denaturation at 95 °C for 30 s, annealing at 60 °C for 30 s, and extension at 72 °C for 30s; and an extension step of 72 °C for 5 min finally. The amplified PCR products were visualized by gel electrophoresis on 1% agarose gels.

Screening and characterization of X chromosome-specific markers in mandarin fish (Siniperca chuatsi).
Aquaculture. (IF: 5.14)

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Aquaculture
Volume 565, 25 February 2023, 739147

Screening and characterization of sex-specific markers by NGS sequencing in *Spinibarbus hollandi* with implication of XY sex determination system

Chong Han, Wenwei Huang, Suhan Peng, Jiangwei Zhou, Huawei Zhan, Lin Gui, Wenjun Li, Qiang Li

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Abstract

Sex-specific markers are critical for understanding sex determination mechanism and development of unisexual breeding in fish. *Spinibarbus hollandi* is an important commercial aquaculture species in southeastern China. Here, through whole genome

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2.4. Development and verification of male-specific sequences

According to the obtained sex-specific sequences, a total of 20 primer pairs were designed using Primer 5.0. These primers were first verified in DNA samples of eight female and eight male *S. hollandi*. Then, the valid primers were further verified in DNA samples of another twenty four females and twenty four males. The PCR amplification reaction was carried out in a total of 10 μl reaction system, including 5 μl 2 x Taq Master Mix (GDSBIO, China), 0.5 μl each primer (10 uM), 0.5 μl DNA template and 3.5 μl ddH_2O. The PCR amplification conditions include 5 min at 95 °C for pre-denaturation, following by 33 cycles 30 s at 95 °C, 30 s at 55 °C, 30 s at 72 °C, and a final extension for 5 min at 72 °C. Gel electrophoresis was used to detect the PCR products by 1.2% agarose gel.

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STING signaling sensing of DRP1-dependent mtDNA release in kupffer cells contributes to lipopolysaccharide-induced liver injury in mice

Qin Zhang [1], Jiayi Wei [1], Zhuanhua Liu [1], Xiaoxia Huang [1], Maomao Sun [1], Wujiang Lai [2], Zhenfeng Chen [1], Jie Wu [3], Yanjia Chen [4], Xiaohua Guo [1], Qiaobing Huang [5]

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Corrigendum to "STING signaling sensing of DRP1-dependent mtDNA release in kupffer cells contributes to lipopolysaccharide-induced liver injury in mice" [Redox Biol. 54 (2022) 102367/PMID:35724543].

Zhang Q, Wei J, Liu Z, Huang X, Sun M, Lai W, Chen Z, Wu J, Chen Y, Guo X, Huang Q.

Redox Biol. 2023 Jun;62:102664. doi: 10.1016/j.redox.2023.102664. Epub 2023 Mar 12.

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Abstract

Aberrant pro-inflammatory activation of Kupffer cells (KCs) is strongly involved in the pathogenesis of

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2.6. Quantitative real-time PCR

Total RNA from KCs was isolated with Trizol reagent. 500 ng of total RNA was reverse-transcribed into cDNA by using the RT-PCR Mix for qPCR kit (R1031, GDSBio) in which the genomic DNA was removed by DNase digestion. Real-time qPCR was conducted on the 7500 Real-Time PCR System (Applied Biosystems) with a Power Green qPCR Mix (P2102a, GDSBio) according to the manufacturer's procedures. The results of relative expression of mRNA of IFN-β, TNF-α and IL-1β were normalized to the Ct value of GAPDH in each sample. The primers for qPCR analysis of sequences were presented in Supplementary Table 1.

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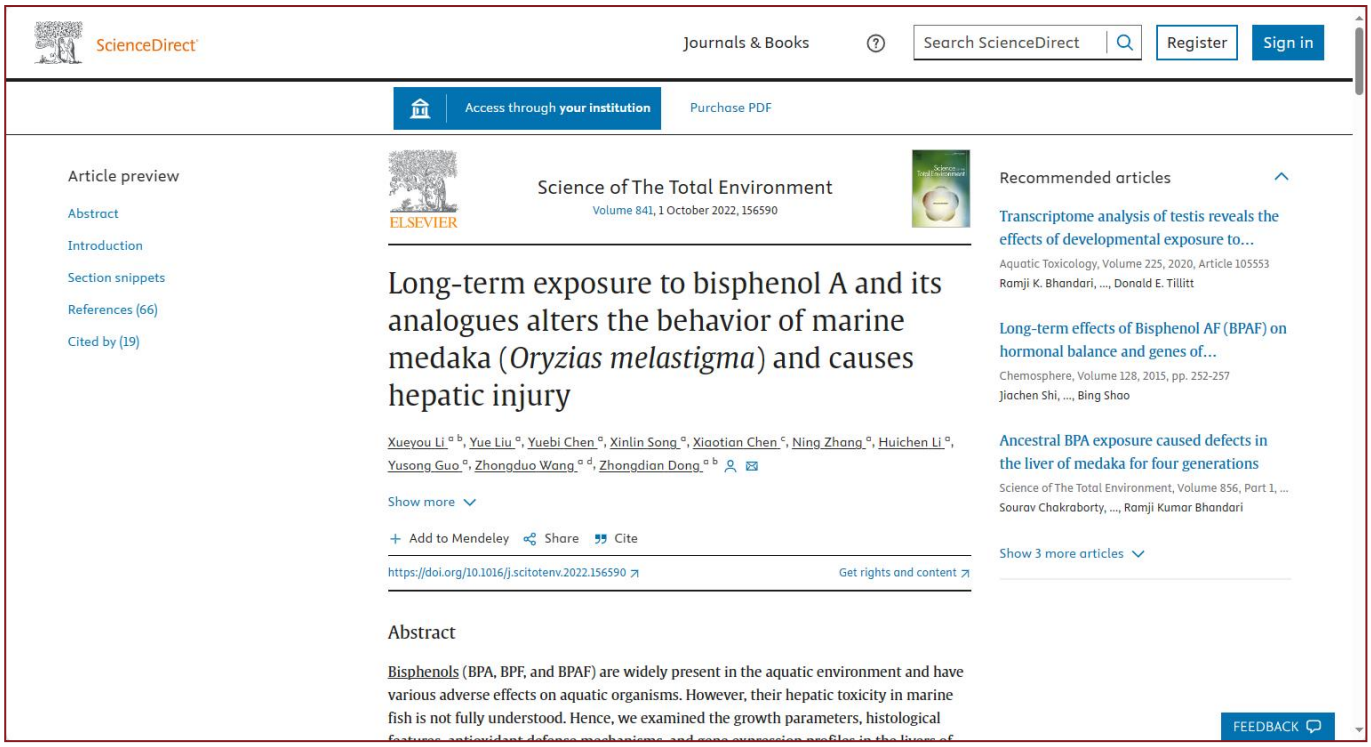
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Science of The Total Environment
Volume 841, 1 October 2022, 156590

Long-term exposure to bisphenol A and its analogues alters the behavior of marine medaka (*Oryzias melastigma*) and causes hepatic injury

Xueyou Li [a b], Yue Liu [a], Yuebi Chen [a], Xinlin Song [a], Xiaotian Chen [c], Ning Zhang [a], Huichen Li [a], Yusong Guo [a], Zhongduo Wang [a d], Zhongdian Dong [a b]

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Abstract

Bisphenols (BPA, BPF, and BPAF) are widely present in the aquatic environment and have various adverse effects on aquatic organisms. However, their hepatic toxicity in marine fish is not fully understood. Hence, we examined the growth parameters, histological

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2.7. Quantitative real-time polymerase chain reaction (qPCR)

Three liver samples were randomly selected from each treatment for total RNA isolation, cDNA synthesis, and quantitative real-time polymerase chain reaction (qPCR). qPCR was performed using a Roche LightCycler 96 (Roche, Basel, Switzerland). The total reaction system was 15 μL, including 7.5 μL of 2 × SYBR Premix Ex Taq II (GDSBio, Guangzhou, China), 0.3 μL of each primer (10 μM), 2 μL of cDNA, and 4.9 μL of ddH_2O. The reaction program adopted a three-step method: pre-denaturation at 95 °C for 180 s, followed by 40 cycles of 10 s at 95 °C, 30 s at 60 °C, and 30 s at 72 °C. A dissociation curve analysis was performed at the end of amplification to determine target specificity. The relative expression levels were measured according to the threshold cycle value and normalized using the −ΔΔCt method. *Rps4x* was used as reference gene owing to its stable expression in liver samples under different treatment conditions. All primer sequences used for qPCR are listed in Table S1.

Long-term exposure to bisphenol A and its analogues alters the behavior of marine medaka (Oryzias melastigma) and causes hepatic injury.
Science of The Total Environment. (IF: 10.75)

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ACS Appl Mater Interfaces. 2023 Nov 1. doi: 10.1021/acsami.3c11227. Online ahead of print.

CpG-Conjugated Silver Nanoparticles as a Multifunctional Nanomedicine to Promote Macrophage Efferocytosis and Repolarization for Atherosclerosis Therapy

Cui Tang [1 2], Hui Wang [2], Lina Guo [1], Chan Zou [2], Jianming Hu [3], Hanyong Zhang [4], Wenhu Zhou [1 4 5], Guoping Yang [1 2 6 7]

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Abstract

Atherosclerosis (AS) is a major contributor to cardiovascular diseases, necessitating the development of novel therapeutic strategies to alleviate plaque burden. Macrophage efferocytosis, the process by which macrophages clear apoptotic and foam cells, plays a crucial role in plaque regression. However, this process is impaired in AS lesions due to the overexpression of CD47, which produces a "do not eat me" signal. In this study, we investigated the potential of CpG, a toll-like receptor 9 agonist, to enhance macrophage efferocytosis for AS therapy. We demonstrated that CpG treatment promoted the engulfment of CD47-positive apoptotic cells and foam cells by macrophages. Mechanistically, CpG induced a metabolic shift in macrophages characterized by enhanced fatty acid oxidation and de novo lipid biosynthesis, contributing to its pro-efferocytic effect. To enable in vivo application, we conjugated CpG on silver nanoparticles (AgNPs) to form CpG-AgNPs, which could protect CpG from

reaction test (RT-PCR) were purchased from Sangon Biotechnology Co., Ltd. (Shanghai, China). GSH was provided by Yuanye Bio-Technology Co., Ltd. (Shanghai, China). The 2′,7′-dichlorodihydro-fluorescein diacetate (DCFH-DA), a cytosolic reactive oxygen species (ROS) probe, was purchased from Sigma-Aldrich Co., Ltd. (St. Louis, USA). SYBR green was purchased from Dongsheng Biotech Co., Ltd. (Guangzhou, China). The RevertAid First Strand cDNA synthesis kit and CellTracker deep red dye were from Thermo Fisher Scientific Co., Ltd. (MA, USA). Cell-tracker green CMFDA was from Maokang

CpG-Conjugated Silver Nanoparticles as a Multifunctional Nanomedicine to Promote Macrophage Efferocytosis and Repolarization for Atherosclerosis Therapy. ACS Applied Materials & Interfaces. (IF: 9.50)

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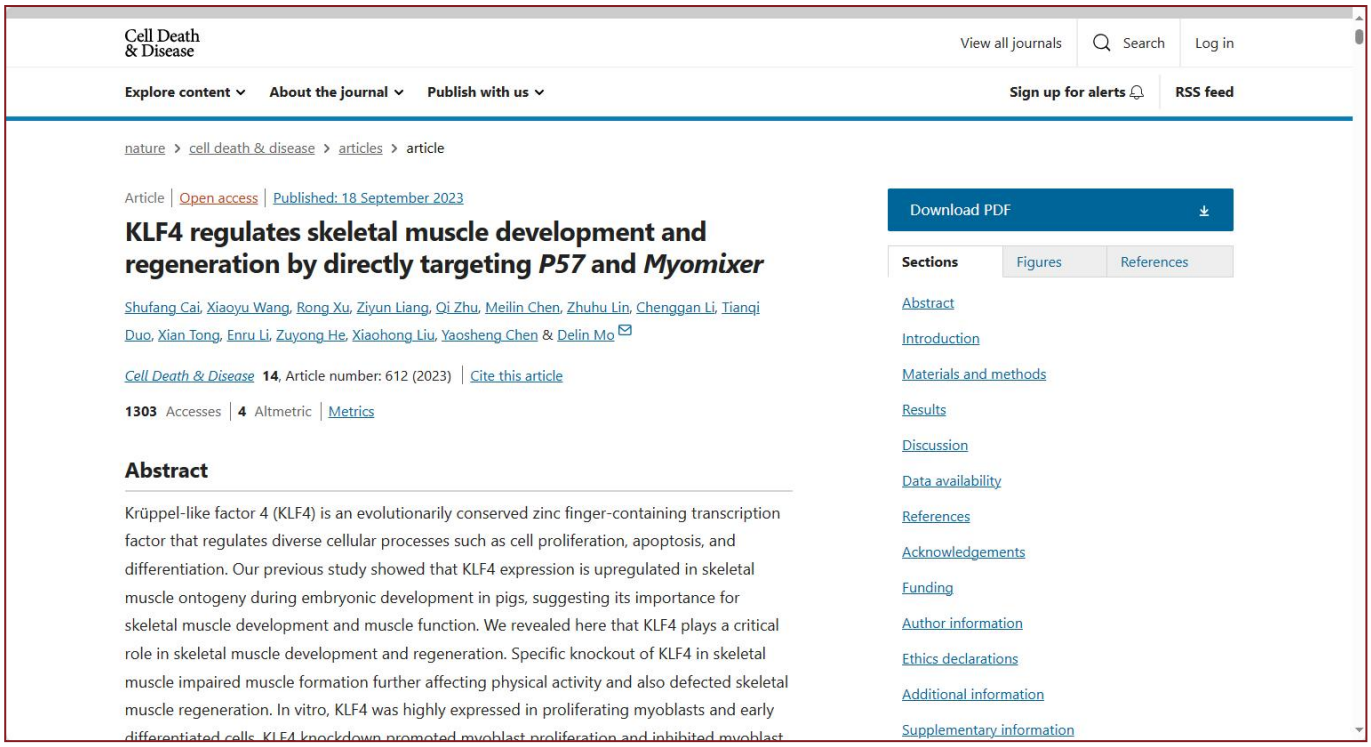

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KLF4 regulates skeletal muscle development and regeneration by directly targeting *P57* and *Myomixer*

Shufang Cai, Xiaoyu Wang, Rong Xu, Ziyun Liang, Qi Zhu, Meilin Chen, Zhuhu Lin, Chenggan Li, Tianqi Duo, Xian Tong, Enru Li, Zuyong He, Xiaohong Liu, Yaosheng Chen & Delin Mo

Cell Death & Disease **14**, Article number: 612 (2023) | Cite this article

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Abstract

Krüppel-like factor 4 (KLF4) is an evolutionarily conserved zinc finger-containing transcription factor that regulates diverse cellular processes such as cell proliferation, apoptosis, and differentiation. Our previous study showed that KLF4 expression is upregulated in skeletal muscle ontogeny during embryonic development in pigs, suggesting its importance for skeletal muscle development and muscle function. We revealed here that KLF4 plays a critical role in skeletal muscle development and regeneration. Specific knockout of KLF4 in skeletal muscle impaired muscle formation further affecting physical activity and also defected skeletal muscle regeneration. In vitro, KLF4 was highly expressed in proliferating myoblasts and early differentiated cells. KLF4 knockdown promoted myoblast proliferation and inhibited myoblast

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Supplementary information

RNA extraction and Real-time quantitative PCR

Total RNA was extracted from cultured C2C12 cells and regenerating TA muscles using Trizol Reagent (Invitrogen). Then, cDNA was synthesized from 1 μg total RNA using StarScript II First-strand cDNA Synthesis Mix (Genestar, Beijing, China). Real-time quantitative PCR (qPCR) analyses were performed on LightCycler 480 II (Roche, Basel, Switzerland) using SYBR Green qPCR Mix (GDSBio, Guangzhou, China), with GAPDH as an internal control for normalization. Primers are listed in Table S3.

KLF4 regulates skeletal muscle development and regeneration by directly targeting P57 and Myomixer. Cell Deadth & Disease. (IF: 9.00)

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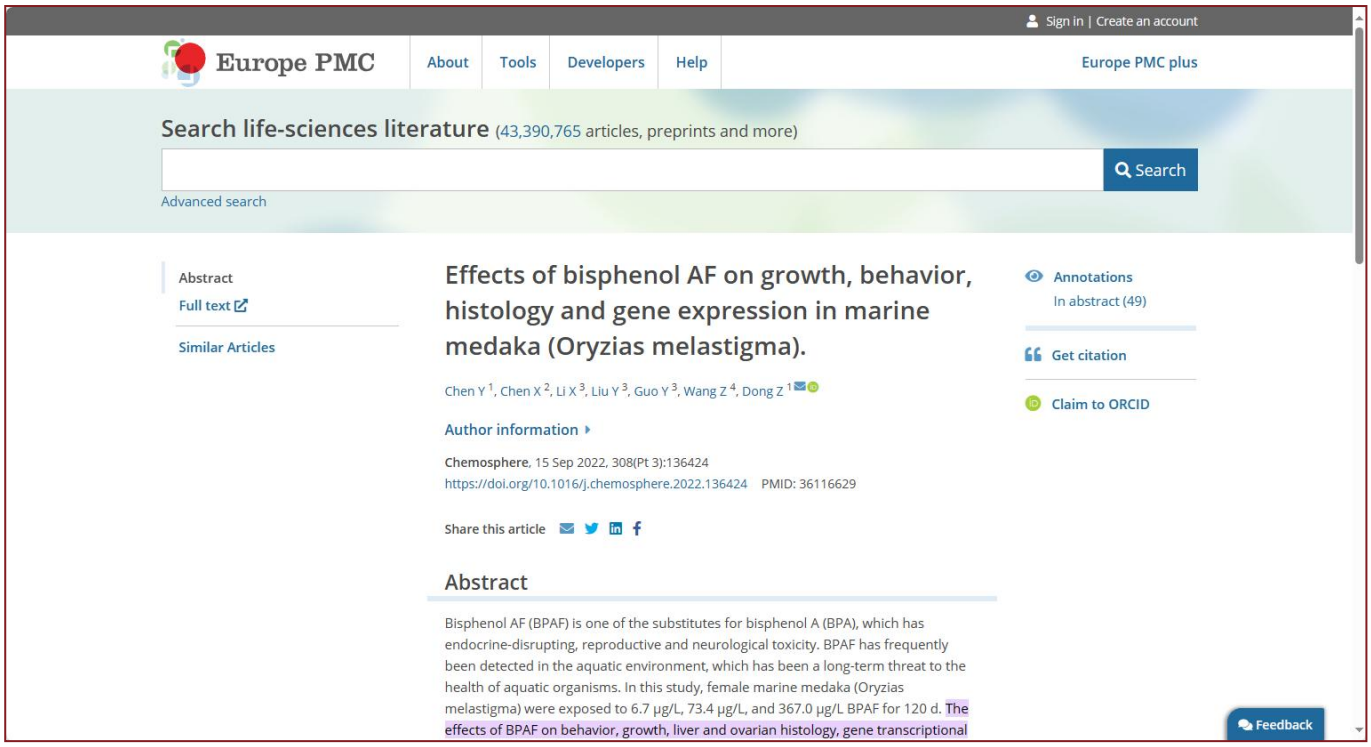

scriptional expression levels of target genes (Li et al., 2021). Quantitative polymerase chain reaction (qPCR) was performed using the SYBR® Green qPCR Mix (Dongsheng Biotech Co., Ltd., Guangzhou, China). All reactions were performed on the LightCycler® 96 PCR system (Roche, Basel, Switzerland). The list of primers is shown in Table S1. The PCR system (15 μL) contained 7.5 μL of 2 x SYBR® Green qPCR Mix[a], 0.4 μL of each forward and reverse primers (10 μM), 1.5 μL of cDNA samples, and 5.2 μL of nuclease-free water. The qPCR reaction conditions were as

Effects of bisphenol AF on growth, behavior, histology and gene expression in marine medaka (Oryzias melastigma). Chemosphere. (IF: 8.94)

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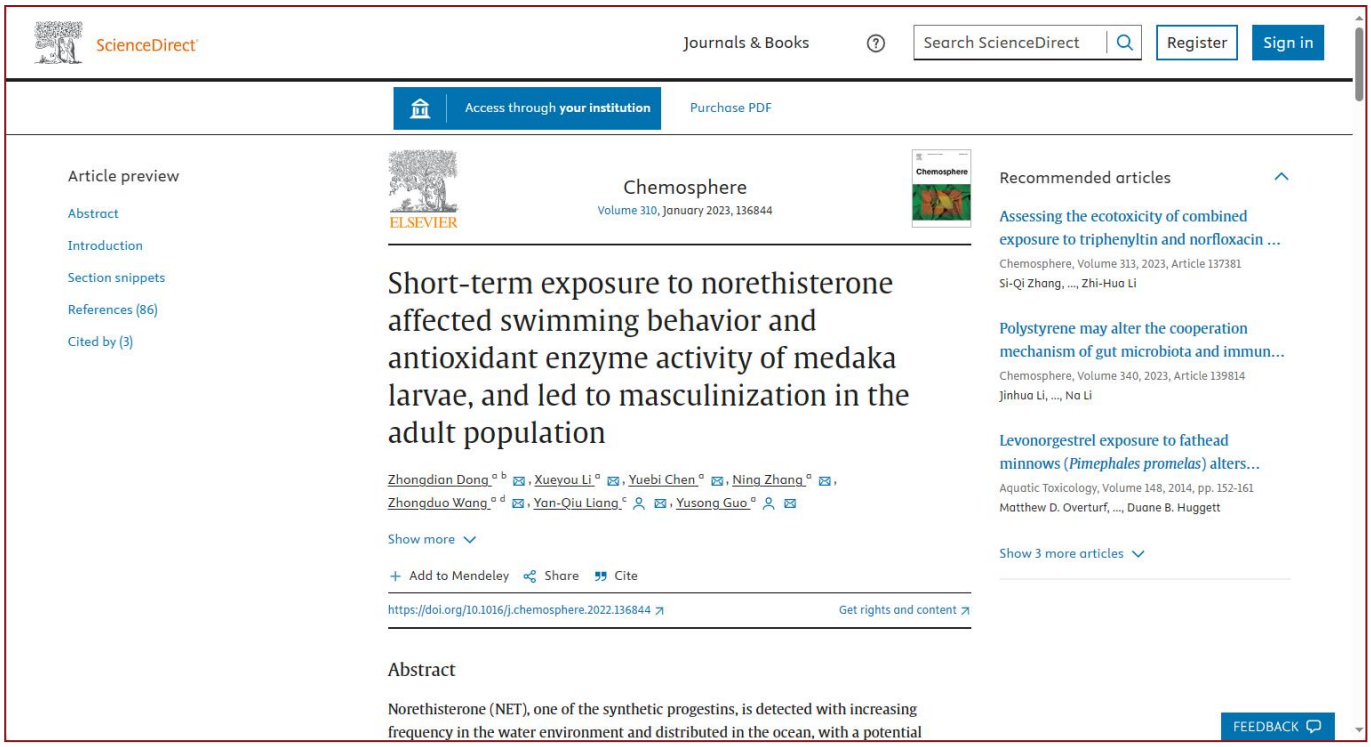
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Chemosphere
Volume 310, January 2023, 136844

Short-term exposure to norethisterone affected swimming behavior and antioxidant enzyme activity of medaka larvae, and led to masculinization in the adult population

Zhongdian Dong, Xueyou Li, Yuebi Chen, Ning Zhang, Zhongduo Wang, Yan-Qiu Liang, Yusong Guo

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Norethisterone (NET), one of the synthetic progestins, is detected with increasing frequency in the water environment and distributed in the ocean, with a potential

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beta-2 (*actb2*) and glyceraldehyde-3-phosphate dehydrogenase (*gadph*) were used as internal reference genes (Dong et al., 2022). Roche LightCycler 96 (Roche, Basel, Switzerland) was used to perform the qPCR reaction, and the qPCR reaction reagent was Power Green qPCR Mix (GDSBio, Guangzhou, China). The system formulation and reaction procedure of qPCR refer to our previous study (Li et al., 2022). The relative mRNA expression level of target gene was transformed as Log_2 according to the $2^{-\Delta\Delta Ct}$ method (Livak and Schmittgen, 2001). Graph-Pad Prism 9 (GraphPad Software, Inc., La Jolla, CA, USA) was used to analyze and graph the data (expressed as Log_2 form).

Short-term exposure to norethisterone affected swimming behavior and antioxidant enzyme activity of medaka larvae, and led to masculinization in the adult population.
Chemosphere. (IF: 8.94)

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Comparative Study > Front Immunol. 2022 Jan 27:13:778915. doi: 10.3389/fimmu.2022.778915. eCollection 2022.

Molecular Identification of *Nocardia seriolae* and Comparative Analysis of Spleen Transcriptomes of Hybrid Snakehead (*Channa maculata* Female × *Channa argus* Male) With Nocardiosis Disease

Ning Zhang [1], Hairui Zhang [2], Zhongdian Dong [1], Wei Wang [1 3 4]

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PMID: 35154103 PMCID: PMC8828968 DOI: 10.3389/fimmu.2022.778915
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Abstract

Hybrid snakehead (*Channa maculata* female × *Channa argus* male) is a new freshwater aquaculture fish species in southern China. During intensive aquaculture, hybrid snakeheads are often infected by *Nocardia seriolae*. In this study, hybrid snakehead infected suspiciously by *N. seriolae* in an artificial breeding pond were examined. Diseased hybrid snakeheads swam slowly without food intake, and the clinical symptoms included skin wound, anal swelling and ascites, and white granulomatous in liver, spleen, and kidney of fish. Through bacterial isolation, 16S rDNA sequencing, fluorescence *in situ* hybridization (FISH) and artificial infection experiment, the pathogen was identified as *N. seriolae*. Furthermore, the spleen samples from diseased and healthy male hybrid snakeheads in the same pond were used for RNA-Seq analysis. A total of 3,512 unique transcripts (unigenes) were identified as

qPCR Validation

In order to validate the results of the RNA-Seq, twenty DEGs were randomly selected for validation by qPCR. Primers were designed according to the transcriptome sequences (**Supplementary Table 1**). qPCR was performed on Roche LightCycler 96 (Roche, Forrentrasse, Switzerland) using SYBR® Green qPCR Mix (GDSBio, Guangzhou, China). The reaction was carried out using a qPCR mixture of 15.0 µL, containing 7.5 µL 2 X SYBR® Green qPCR, 0.6 µL of each forward and reverse primer, 1.5 µL cDNA and 4.8 µL ddH_2O. qPCR amplification was done as follows: 180 s at 95°C for pre-incubation, followed by 40 cycles at 95°C for 15 s, 60°C for 15 s and 72°C for 30 s. Dissociation and melting curves of qPCR products were performed, and results were analyzed. *β-actin* and *ef2b* were used as reference genes to determine relative expression (5). The transcriptional data were

Molecular Identification of Nocardia seriolae and Comparative Analysis of Spleen Transcriptomes of Hybrid Snakehead (Channa maculata Female × Channa argus Male) With Nocardiosis Disease. Frontiers in Immunology. (IF: 8.79)

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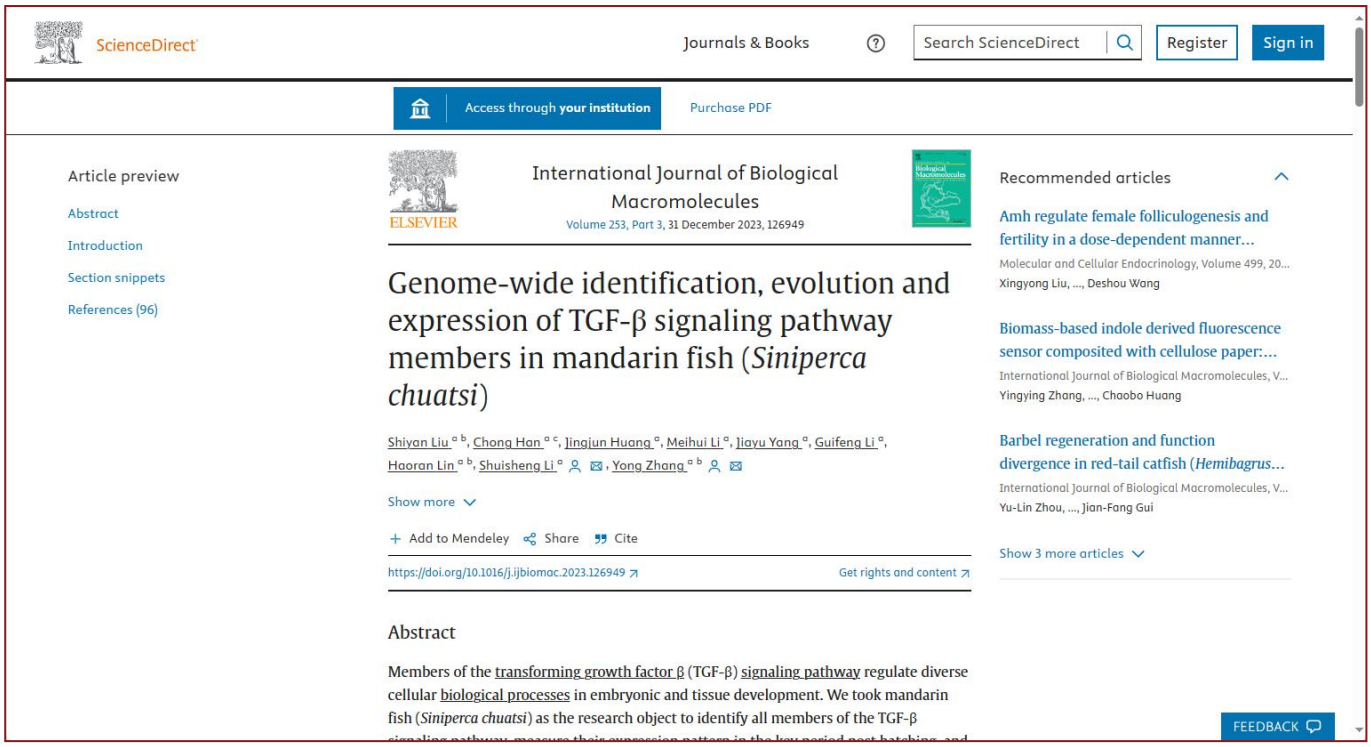

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ELSEVIER International Journal of Biological Macromolecules
Volume 253, Part 3, 31 December 2023, 126949

Genome-wide identification, evolution and expression of TGF-β signaling pathway members in mandarin fish (*Siniperca chuatsi*)

Shiyan Liu [a b], Chong Han [a c], Jingjun Huang [a], Meihui Li [a], Jiayu Yang [a], Guifeng Li [a], Haoran Lin [a b], Shuisheng Li [a], Yong Zhang [a b]

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Abstract

Members of the transforming growth factor β (TGF-β) signaling pathway regulate diverse cellular biological processes in embryonic and tissue development. We took mandarin fish (*Siniperca chuatsi*) as the research object to identify all members of the TGF-β

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According to the genome and transcriptome data of mandarin fish, the open reading frames (ORFs) of sex-associated genes (*amh*, *amhr2*, *gdf9*, *bmp15*, *gsdf*, *gdf3*, *smad1*, *smad5*, *smad9*, *inha*) were predicted, and gene-specific primers were designed using Primer 5.0 software (Table S1). Then, qRT–PCR was conducted using SYBR Green qPCR Mix (GDSBio, China) and performed on a Roche LightCycler 480 real-time PCR system. The qRT–PCR program was as follows: predenaturation at 95 °C for 3 min; followed by 45 cycles of 95 °C for 10 s, 58 °C for 20 s, and 72 °C for 15 s; and a final extension at 72 °C for 5 min, ending with a dissociation curve process. All qRT-PCRs used *β-actin* as the internal control and were carried out in triplicate to confirm the results. The specificity of each primer amplification was conducted with the dissociation curve. Under a fivefold cDNA dilution series, the qPCR

Genome-wide identification, evolution and expression of TGF-β signaling pathway members in mandarin fish (Siniperca chuatsi).
International Journal of Biological Macromolecules. (IF: 8.20)

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ELSEVIER International Journal of Biological Macromolecules
Volume 254, Part 1, January 2024, 127667

Molecular characterization and expression analysis of nine toll like receptor (TLR) genes in *Scortum barcoo* under *Streptococcus agalactiae* infection

Songze Gao [b], Wenwei Huang [a], Suhan Peng [a], Jiangwei Zhou [a], Huawei Zhan [a], Tongfu Lu [a], Weiqian Liang [a], Junwu Li [a], Yuying Zhang [a], Wenjun Li [a], Chong Han [a], Qiang Li [a]

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Abstract

Toll like receptors (TLRs) are important pattern recognition receptors participating in innate immune system. Up to now, no TLR has been identified in Jade perch (*Scortum barcoo*). In this study, we successfully identified 9 members of TLRs from the Jade perch.

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Total RNA was extracted from all obtained tissues using a Trizol RNA extraction kit (Invitrogen, USA) following the manufacturer's instructions. The quantity and quality of RNA were further detected using Nanodrop 2000c (ThermoFisher, USA). Then, all cDNA templates were synthesized using RT-PCR Mix for qPCR (GDSBIO, China) and then stored at −20 °C.

To detect expression profiles of SbTLRs, quantitative real time PCR (qRT-PCR) reaction was performed using the SYBR Green qPCR Mix (GDSBIO, China) on a LightCycle 480 System (Roche, Germany). All primers used in qRT-PCR reaction were designed by Primer 3.0 (Table 1) and further validated using agarose gel electrophoresis and Sanger sequencing. All qRT-PCR reactions were performed in a volume of 10 μL, containing 0.5 μL cDNA, 0.5 μL of each primer (10 μM), 5 μL SYBR Green qPCR Mix, and 3.5 μL of ddH_2O. The PCR cycling conditions are pre-

Molecular characterization and expression analysis of nine toll like receptor (TLR) genes in Scortum barcoo under Streptococcus agalactiae infection.
International Journal of Biological Macromolecules. (IF: 8.20)

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PLoS Pathog. 2021 Feb 26;17(2):e1008690. doi: 10.1371/journal.ppat.1008690. eCollection 2021 Feb.

Inhibition of anti-viral stress granule formation by coronavirus endoribonuclease nsp15 ensures efficient virus replication

Bo Gao [1], Xiaoqian Gong [1 2], Shouguo Fang [3], Wenlian Weng [1], Huan Wang [1], Hongyan Chu [1], Yingjie Sun [1], Chunchun Meng [1], Lei Tan [1], Cuiping Song [1], Xusheng Qiu [1], Weiwei Liu [1], Maria Forlenza [2], Chan Ding [1 4], Ying Liao [1]

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Abstract

Cytoplasmic stress granules (SGs) are generally triggered by stress-induced translation arrest for storing mRNAs. Recently, it has been shown that SGs exert anti-viral functions due to their involvement in protein synthesis shut off and recruitment of innate immune signaling intermediates. The largest RNA viruses, coronaviruses, impose great threat to public safety and animal health; however, the significance of SGs in coronavirus infection is largely unknown. Infectious Bronchitis Virus (IBV) is the first identified coronavirus in 1930s and has been prevalent in poultry farm for many years. In this study, we provided evidence that IBV overcomes the host antiviral response by inhibiting SGs formation via the virus-encoded endoribonuclease nsp15. By immunofluorescence analysis, we observed that IBV infection not only did not trigger SGs formation in approximately 80% of the

Quantitative RT-PCR analysis

Total cellular RNAs were extracted using Trizol reagent (Ambion). cDNAs were synthesized from 2μg total RNA using oligo(dT) primers and M-MLV reverse transcriptase system (Promega). cDNA was used as template for quantitative PCR using a Bio-Rad CFX-96 real time PCR apparatus and SYBR green master mix (Dongsheng Biotech). PCR conditions were as follow: an initial denaturation at 94°C for 3 min, 40 cycles of 94°C for 15 s, 60°C for 15 s and 72°C for 20 s. The specificity of the amplified PCR products was confirmed by melting curve analysis after each reaction. The primers used were: for human *IFN-β*, 5'-GCTTGGATTC

Inhibition of anti-viral stress granule formation by coronavirus endoribonuclease nsp15 ensures efficient virus replication.
Plos Pathogens. (IF: 7.46)

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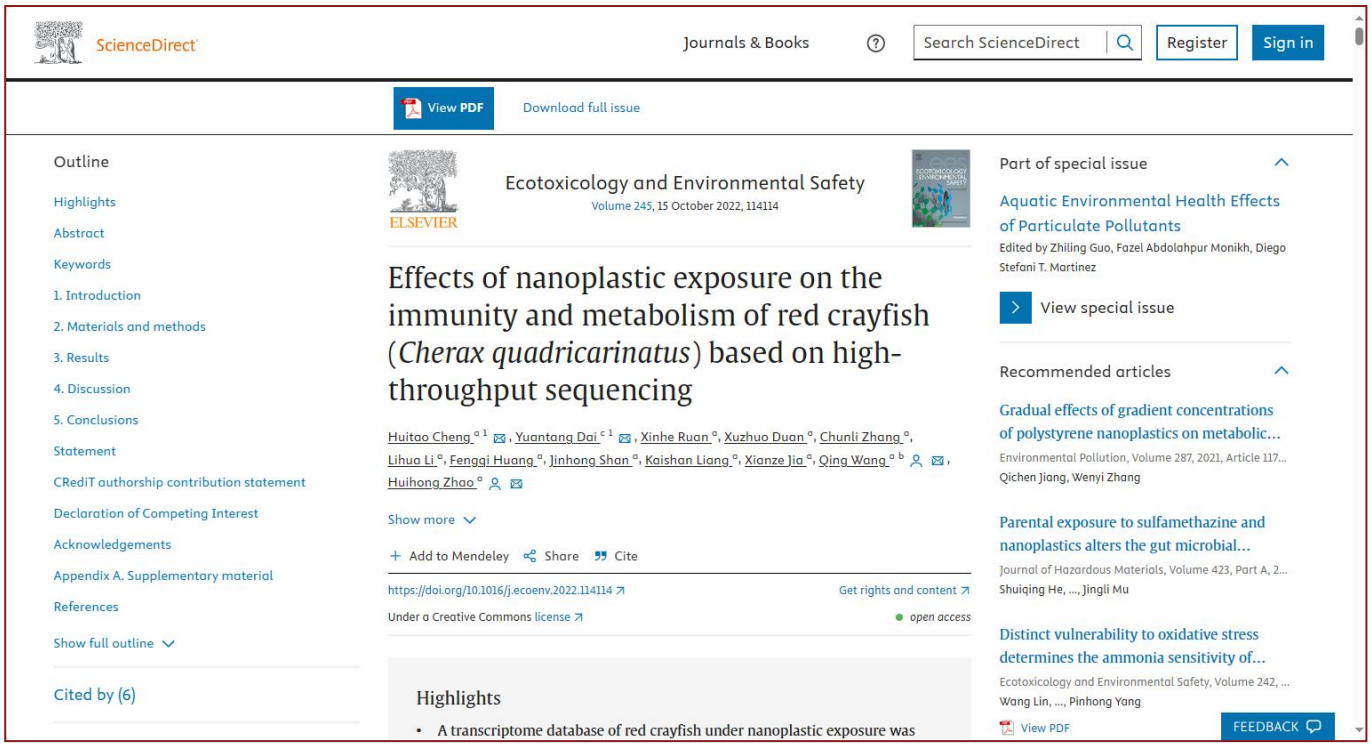

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Ecotoxicology and Environmental Safety
Volume 245, 15 October 2022, 114114

ELSEVIER

Effects of nanoplastic exposure on the immunity and metabolism of red crayfish (*Cherax quadricarinatus*) based on high-throughput sequencing

Huitao Cheng [a 1], Yuantang Dai [c 1], Xinhe Ruan [a], Xuzhuo Duan [a], Chunli Zhang [a], Lihua Li [a], Fenggi Huang [a], Jinhong Shan [a], Kaishan Liang [a], Xianze Jia [a], Qing Wang [a b], Huihong Zhao [a]

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Highlights

- A transcriptome database of red crayfish under nanoplastic exposure was

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2.3.4. Verification of DEGs by quantitative real-time PCR (qRT-PCR)

To verify the reliability of the transcriptome data, 12 differentially expressed genes were selected for qRT-PCR validation. Based on the 12 genes and β-actin sequences, Premier6 software were used to design specific primers for qRT-PCR analysis (Table S1). The PCR reaction system was 10 μL consisting of 5 μL 2 × SYBR Ex Taq (Guangzhou Dongsheng Biotechnology Co., Ltd.), 0.2 μL of each gene-specific primer (10 nmol), 1 μL cDNA and 3.6 μL ribonuclease-free water composition. Cycling conditions were 3 min at 94 °C; 40 cycles of 94 °C for 15 s, 60 °C for 15 s, and 72 °C for 20 s. The relative expression was calculated by the $2^{-\Delta\Delta CT}$ method with β-actin gene as the internal reference gene.

Effects of nanoplastic exposure on the immunity and metabolism of red crayfish (Cherax quadricarinatus) based on high-throughput sequencing. Ecotoxicology and Environmental Safety. (IF: 7.13)

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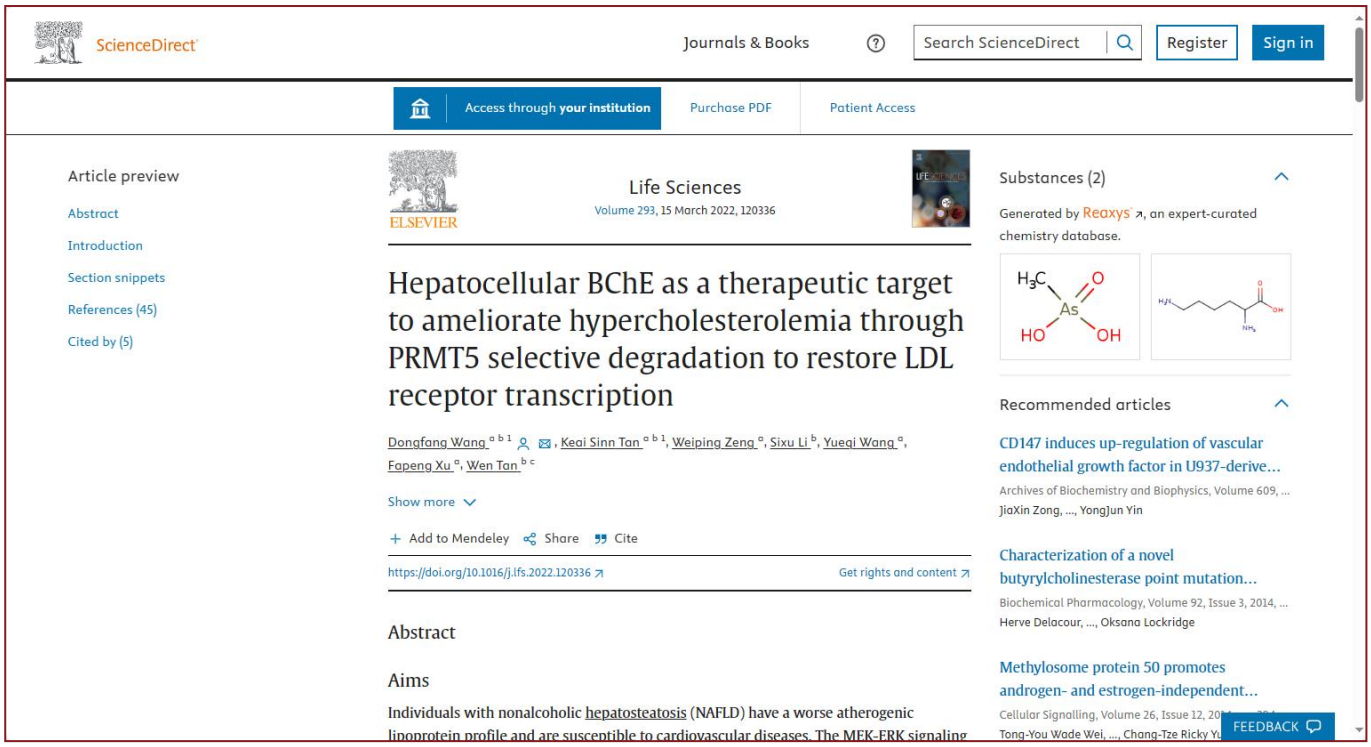

Total RNA was extracted from Aml-12 cells using TRIzol Reagent (Invitrogen, 15596026) as described by the manufacturer. RNA integrity was determined by agrose eletrophorosis, and RNA concentration was measured by NanoDrop 2000. Reverse transcription was performed to synthesize single-stranded cDNA using 5 μg RNA as the template according the protocol of the manufacturer (Hifair® III 1st Strand cDNA Synthesis Kit (gDNA digester plus), 11139ES60, Yeasen Biotechnology). Real-time PCR was performed with Power Green qPCR Mix No ROX (P2104, GDSbio, China) on the Roche LightCycler® 96 Instrument. β-actin was used as the internal control to normalize the data. The amplification program was as follows, 95 °C for 3 min, and 40 cycles at 95 °C for 15 s, 60 °C for 15 s, 72 °C for 20 s. Dissociation curves were analyzed at the end of the amplification. The fold change of gene

Hepatocellular BChE as a therapeutic target to ameliorate hypercholesterolemia through PRMT5 selective degradation. Life Sciences. (IF: 6.78)

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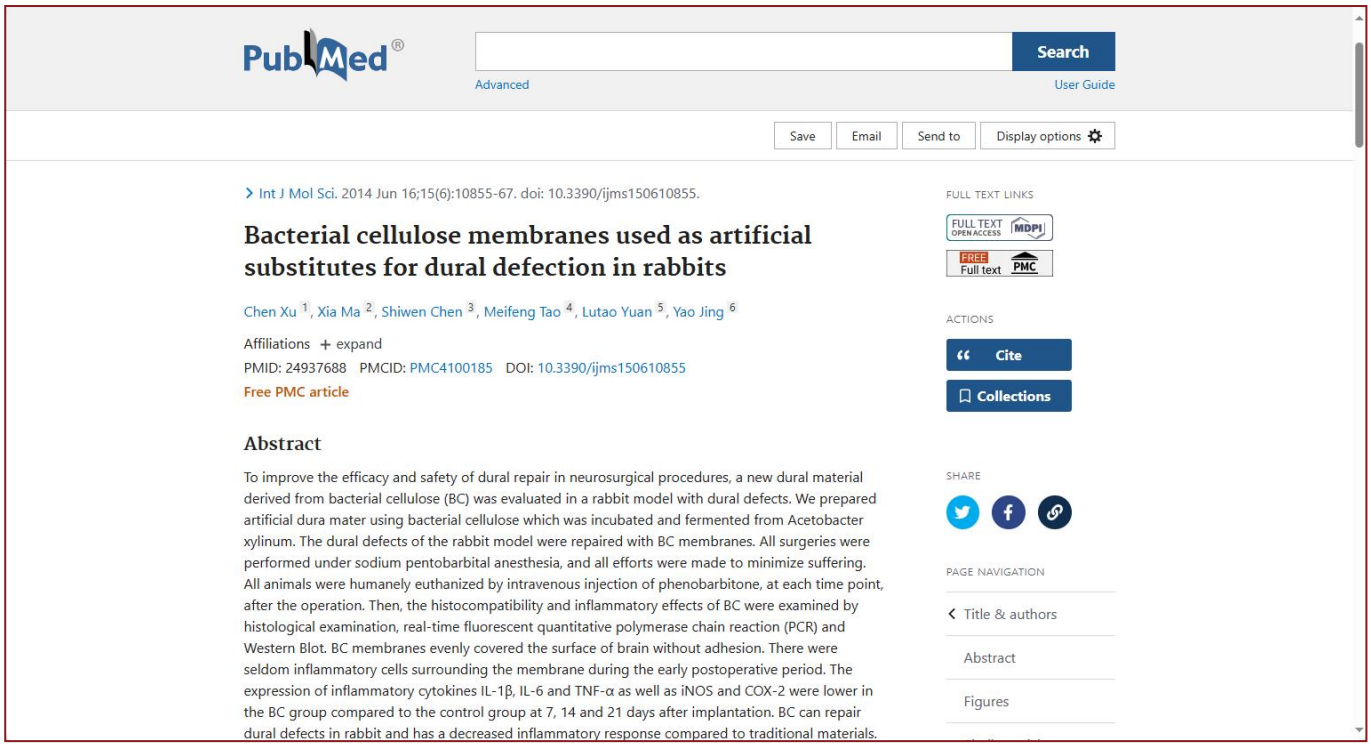

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Int J Mol Sci. 2014 Jun 16;15(6):10855-67. doi: 10.3390/ijms150610855.

Bacterial cellulose membranes used as artificial substitutes for dural defection in rabbits

Chen Xu [1], Xia Ma [2], Shiwen Chen [3], Meifeng Tao [4], Lutao Yuan [5], Yao Jing [6]

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PMID: 24937688 PMCID: PMC4100185 DOI: 10.3390/ijms150610855

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Abstract

To improve the efficacy and safety of dural repair in neurosurgical procedures, a new dural material derived from bacterial cellulose (BC) was evaluated in a rabbit model with dural defects. We prepared artificial dura mater using bacterial cellulose which was incubated and fermented from Acetobacter xylinum. The dural defects of the rabbit model were repaired with BC membranes. All surgeries were performed under sodium pentobarbital anesthesia, and all efforts were made to minimize suffering. All animals were humanely euthanized by intravenous injection of phenobarbitone, at each time point, after the operation. Then, the histocompatibility and inflammatory effects of BC were examined by histological examination, real-time fluorescent quantitative polymerase chain reaction (PCR) and Western Blot. BC membranes evenly covered the surface of brain without adhesion. There were seldom inflammatory cells surrounding the membrane during the early postoperative period. The expression of inflammatory cytokines IL-1β, IL-6 and TNF-α as well as iNOS and COX-2 were lower in the BC group compared to the control group at 7, 14 and 21 days after implantation. BC can repair dural defects in rabbit and has a decreased inflammatory response compared to traditional materials.

The PCRs were performed in 20 μL reaction volumes containing 2× SYBR Green Mix 10 μL, Primer Mix 1 μL 9 (DongshengBio, Guangzhou, China), DNA template 1 μL, ddH_2O 8 μL. Denaturation program (95 °C for 2 min), amplification and quantification program repeated 40 times (95 °C for 15 s, 59 °C for 20 s, 72 °C for 20 s with a single fluorescence measurement); Melting curve program (60–95 °C

Bacterial Cellulose Membranes Used as Artificial Substitutes for Dural Defection in Rabbits.
International Journal of Molecular Sciences. (IF: 6.21)

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iScience
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Newcastle-disease-virus-induced ferroptosis through nutrient deprivation and ferritinophagy in tumor cells

Xianjin Kan [1 4], Yuncong Yin [2 4], Cuiping Song [1], Lei Tan [1], Xusheng Qiu [1], Ying Liao [1], Weiwei Liu [1], Songshu Meng [3], Yingjie Sun [1 5], Chan Ding [1 2 5 6]

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- Oncolytic viruses NDV caused tumor cells death through ferroptosis

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Front Oncol. 2022 May 26:12:866289. doi: 10.3389/fonc.2022.866289. eCollection 2022.

Identification and Validation of Novel Immune-Related Alternative Splicing Signatures as a Prognostic Model for Colon Cancer

Yunze Liu [1 2], Lei Xu [3 4], Chuanchuan Hao [1], Jin Wu [3], Xianhong Jia [1], Xia Ding [2], Changwei Lin [5], Hongmei Zhu [1], Yi Zhang [3 4]

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Abstract

Background: Individual immune-related alternative splicing (AS) events have been found to be significant in immune regulation and cancer prognosis. However, a comprehensive analysis of AS events in cancer cells based on immune-related genes (IRGs) has not been performed, and its clinical value is unknown.

Methods: Colon cancer cases with AS data were obtained from TCGA, and then, we identified overall survival-related AS events (OS-ASEs) based on IRGs by univariate analyses. Using Lasso regression, multivariate Cox regression, Kaplan-Meier analysis and nomograms, we constructed an AS risk model based on the calculated risk score. Furthermore, associations of the risk score with clinical and immune features were confirmed through the Wilcoxon rank sum test, association analysis, etc. Finally, by qRT-PCR, cell coculture and CCK-8 analyses, we validated the significance of OS-ASEs in

RNA Extraction and qRT–PCR

Total RNA was extracted from cells and tissues using the TRIzol method (Dongsheng Bio. #R1022) following the protocol. Then, the obtained RNAs were processed for cDNA synthesis. qRT–PCR was then performed using SYBR Green qPCR Mix (Dongsheng Bio. #P2092) and analysed on a Roche LightCycler system. The expression levels of the target genes were normalized based on the expression level of GAPDH. The primer sequences used for amplification and siRNA sequences are listed in the **Supplemental Material**.

Identification and Validation of Novel Immune-Related Alternative Splicing Signatures as a Prognostic Model for Colon Cancer.
Frontiers in Oncology. (IF: 5.74)

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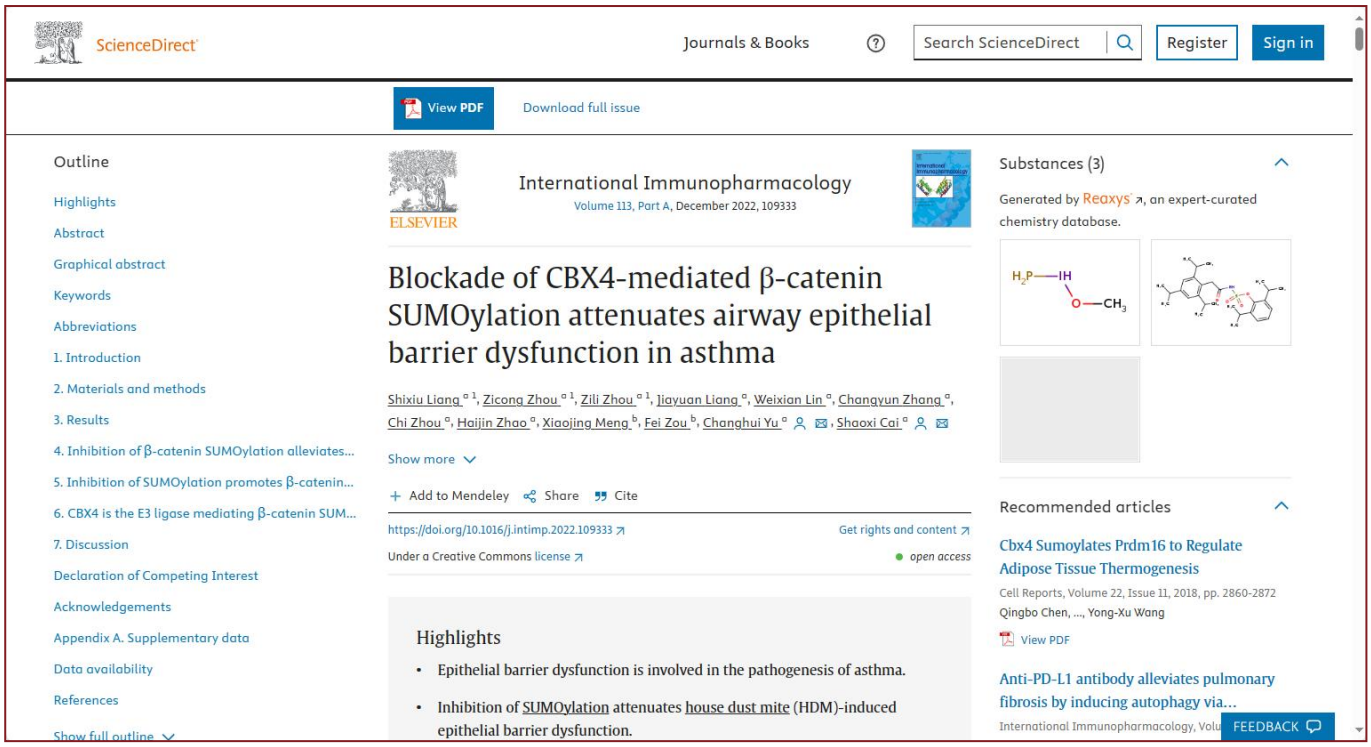
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Outline

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5. Inhibition of SUMOylation promotes β-catenin...
6. CBX4 is the E3 ligase mediating β-catenin SUM...
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International Immunopharmacology
Volume 113, Part A, December 2022, 109333

Blockade of CBX4-mediated β-catenin SUMOylation attenuates airway epithelial barrier dysfunction in asthma

Shixiu Liang [a 1], Zicong Zhou [a 1], Zili Zhou [a 1], Jiayuan Liang [a], Weixian Lin [a], Changyun Zhang [a], Chi Zhou [a], Haijin Zhao [a], Xiaojing Meng [b], Fei Zou [b], Changhui Yu [a], Shaoxi Cai [a]

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Highlights

- Epithelial barrier dysfunction is involved in the pathogenesis of asthma.
- Inhibition of SUMOylation attenuates house dust mite (HDM)-induced epithelial barrier dysfunction.

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Cell Reports, Volume 22, Issue 11, 2018, pp. 2860-2872
Qingbo Chen, ..., Yong-Xu Wang
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International Immunopharmacology, Volu

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2.7. Quantitative PCR (qPCR)

RNA was isolated by a TRIzol Trizol reagent, following the manufacturer's instructions. The cDNA was synthesized via the reverse transcription (Accurate Biology, AG11706). SYBR Green (GDSBio, P2105) was used to perform qPCR using the Real-Time PCR instrument (Bio-Rad). The data were calculated though $2^{-\Delta\Delta Ct}$ method to compare the difference. The following primers were used to amplify the target genes — MMP-9 forward: 5'-CGCCTCTGGAGGTTCGAC-3', reverse: 5'-AACTCACGCGCCAGTAGAAG-3'; VEGF forward: 5'-ATCTTCAAGCCATCCTGTGTGC-3'. reverse: 5'-CAAGGCCCACAGGGATTTTC-3'; TGF-β1 forward: 5'-CGACTCGCCAGAGTGGTTAT-3'. reverse: 5'-CGGTAGTGAACCCGTTGATGT-3'; GAPDH forward: 5'-CCTCCTTCTGCACACATTTGAA-3', reverse: 5'-GAAGATGGTGATGGGATTTC-3'.

Blockade of CBX4-mediated β-catenin SUMOylation attenuates airway epithelial barrier dysfunction in asthma. International Immunopharmacology. (IF: 5.71)

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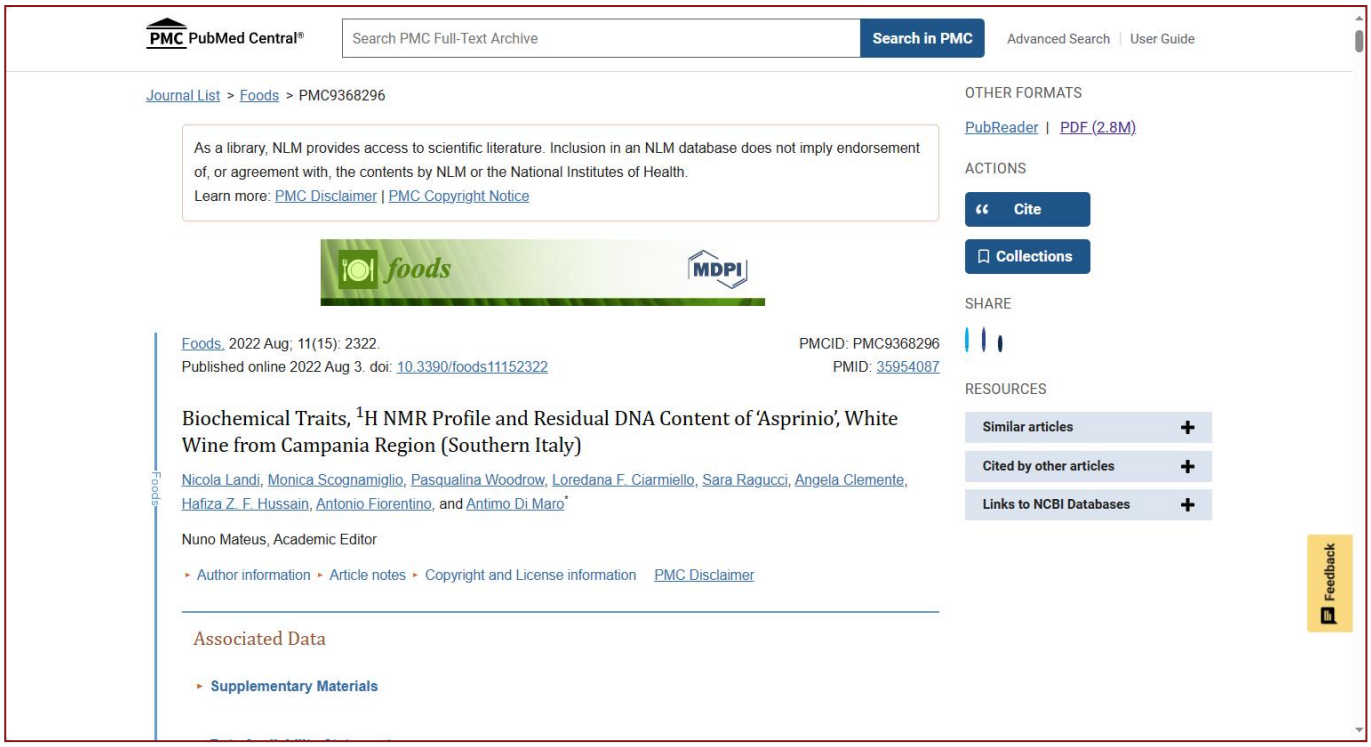

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Foods. 2022 Aug; 11(15): 2322.
Published online 2022 Aug 3. doi: 10.3390/foods11152322

PMCID: PMC9368296
PMID: 35954087

Biochemical Traits, ^{1}H NMR Profile and Residual DNA Content of 'Asprinio', White Wine from Campania Region (Southern Italy)

Nicola Landi, Monica Scognamiglio, Pasqualina Woodrow, Loredana F. Ciarmiello, Sara Ragucci, Angela Clemente, Hafiza Z. F. Hussain, Antonio Fiorentino, and Antimo Di Maro*

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2.7.2. DNA Grapevine and Yeast Quantification

DNA quantification was carried out by quantitative PCR analyses using SYBR Green qPCR Mix (high ROX; GDSBio) by Applied Biosystems™ QuantStudio™ 5 Real-Time PCR System (Thermo Fisher Scientific, Rodano (MI), Italy). The reaction mix (20 µL) consisted of: 2× SYBR Green qPCR Mix, Forward 10 µM for each primer, and DNA template 50 ng. The amplification protocol was: 95 °C initial denaturation step for 3 min, followed by amplification cycles (40×) of denaturing at 95 °C for 10 s, annealing at 60 °C for 10 s and extension at 72 °C for 20 s. Amplification products were visualized on 1.5% (*w*/*v*) agarose gel, using a UV light. Primers used in this study are listed in Table S2.

Biochemical Traits, 1H NMR Profile and Residual DNA Content of 'Asprinio', White Wine from Campania Region (Southern Italy). Foods. (IF: 5.56)

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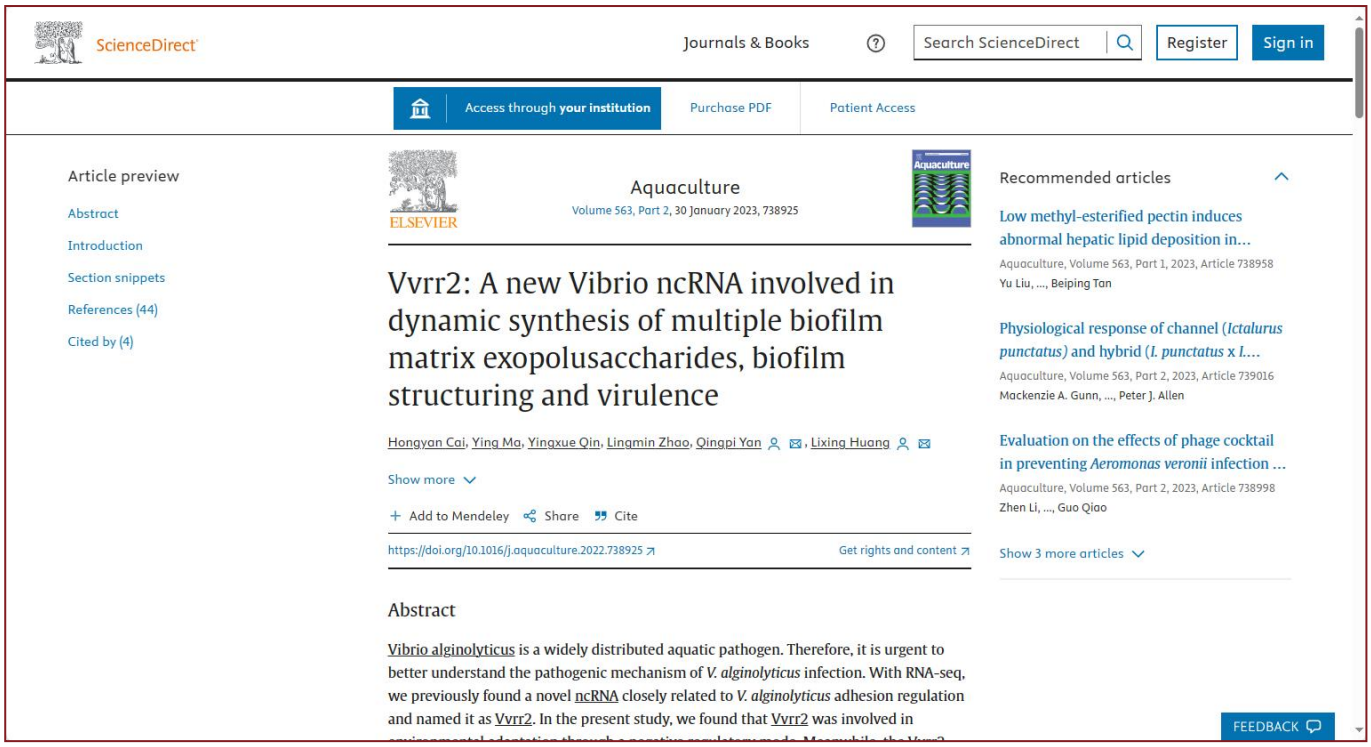
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Aquaculture
Volume 563, Part 2, 30 January 2023, 738925

Vvrr2: A new Vibrio ncRNA involved in dynamic synthesis of multiple biofilm matrix exopolusaccharides, biofilm structuring and virulence

Hongyan Cai, Ying Ma, Yingxue Qin, Linqmin Zhao, Qingpi Yan, Lixing Huang

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Abstract

Vibrio alginolyticus is a widely distributed aquatic pathogen. Therefore, it is urgent to better understand the pathogenic mechanism of *V. alginolyticus* infection. With RNA-seq, we previously found a novel ncRNA closely related to *V. alginolyticus* adhesion regulation and named it as Vvrr2. In the present study, we found that Vvrr2 was involved in

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2.18. Quantitative real-time polymerase chain reaction (qRT-PCR)

qRT-PCR was performed using QuantStudio 6 Flex real-time PCR system (Life Technologies, Carlsbad, CA, USA) together with the Power Green qPCR Mix (Guangzhou Dongsheng Biotech Co., Ltd., China). Primers synthesized by the Xiamen Borui Biotechnology co., LTD (China) were listed in Supplementary Material 1. *gyrB* was used to normalize the gene expression levels. The relative levels of gene expression were calculated by $2^{-\Delta\Delta Ct}$ method (Luo et al., 2016).

Vvrr2: A new Vibrio ncRNA involved in dynamic synthesis of multiple biofilm matrix exopolusaccharides, biofilm structuring and virulence.
Aquaculture. (IF: 5.14)

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J Virol. 2023 Mar 30;97(3):e0001623. doi: 10.1128/jvi.00016-23. Epub 2023 Feb 16.

Newcastle Disease Virus Manipulates Mitochondrial MTHFD2-Mediated Nucleotide Metabolism for Virus Replication

Ning Tang [1 2], Pingyi Chen [3], Changrun Zhao [1], Panrao Liu [4], Lei Tan [2], Cuiping Song [2], Xusheng Qiu [2], Ying Liao [2], Xiufan Liu [4], Tingrong Luo [1 5], Yingjie Sun [2], Chan Ding [1 2 4]

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PMID: 36794935 PMCID: PMC10062132 DOI: 10.1128/jvi.00016-23

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Viruses require host cell metabolic reprogramming to satisfy their replication demands; however, the mechanism by which the Newcastle disease virus (NDV) remodels nucleotide metabolism to support self-replication remains unknown. In this study, we demonstrate that NDV relies on the oxidative pentose phosphate pathway (oxPPP) and the folate-mediated one-carbon metabolic pathway to support replication. In concert with [1,2-$^{13}C_2$] glucose metabolic flow, NDV used oxPPP to promote pentose phosphate synthesis and to increase antioxidant NADPH production. Metabolic flux experiments using [2,3,3-^{2}H] serine revealed that NDV increased one-carbon (1C) unit synthesis flux through the mitochondrial 1C pathway. Interestingly, methylenetetrahydrofolate dehydrogenase (MTHFD2) was upregulated as a compensatory mechanism for insufficient serine availability. Unexpectedly, direct knockdown of enzymes in the one-carbon metabolic pathway, except for

RT-qPCR. Total RNA was extracted from the cell samples using traditional extraction methods and reverse transcribed using M-MLV reverse transcriptase (Promega; M1705). The RT-qPCR probes were obtained using SYBR green qPCR mix (GDSBio, Guangzhou Gongsheng Biotech Co., Ltd.; P2093). The primers targeting different genes were as follows: c-Myc (35), SHMT1 (44), MTHFD1L (45), and MTHFD2 (46). The NDV NP primer sequences were as follows: 5′-CAACAATAGGAGTGGAGTGTCTGA-3′ and downstream primer, 5′-CAGGGTATCG GTGATGTCTTCT-3′. All primer pairs were synthesized by Shanghai Sangon Biotech (Shanghai, China). All samples were standardized according to the mRNA level of β-actin.

Newcastle Disease Virus Manipulates Mitochondrial MTHFD2-Mediated Nucleotide Metabolism for Virus Replication.
Journal of Virology. (IF: 5.10)

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Simultaneous detection of *Salmonella enterica*, *Escherichia coli* O157:H7, and *Listeria monocytogenes* using oscillatory-flow multiplex PCR

Original Paper | Published: 23 March 2011

Volume 173, pages 503–512, (2011) Cite this article

Microchimica Acta

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Abstract

An oscillatory-flow multiplex PCR method in a capillary microfluidic channel has been developed for the simultaneous determination of pre-purified DNA of multiple foodborne bacterial pathogens. The PCR solution passes three temperature zones in an oscillatory manner. The thermal stability and sample evaporation of the microfluidic device were

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The DNA markers, which contain 500, 400, 300, 250, 200, 150, 100 and 50 bp DNA fragments, were from Dongsheng Biotech Co., Ltd. (Guangzhou, China, www.dongshengbio.com).

Simultaneous detection of Salmonella enterica, Escherichia coli O157: H7, and Listeria monocytogenes using oscillatory-flow multiplex PCR.
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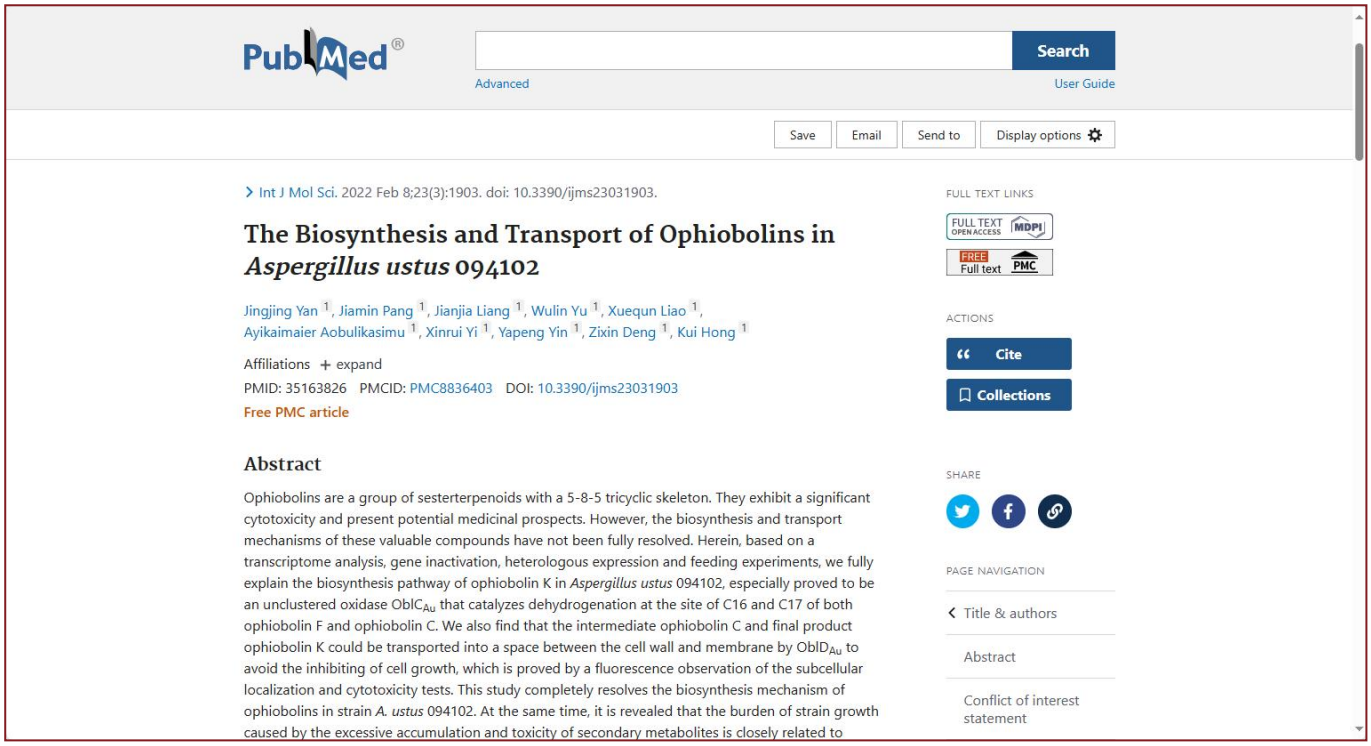

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Int J Mol Sci. 2022 Feb 8;23(3):1903. doi: 10.3390/ijms23031903.

The Biosynthesis and Transport of Ophiobolins in *Aspergillus ustus* 094102

Jingjing Yan [1], Jiamin Pang [1], Jianjia Liang [1], Wulin Yu [1], Xuequn Liao [1], Ayikaimaier Aobulikasimu [1], Xinrui Yi [1], Yapeng Yin [1], Zixin Deng [1], Kui Hong [1]

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Abstract

Ophiobolins are a group of sesterterpenoids with a 5-8-5 tricyclic skeleton. They exhibit a significant cytotoxicity and present potential medicinal prospects. However, the biosynthesis and transport mechanisms of these valuable compounds have not been fully resolved. Herein, based on a transcriptome analysis, gene inactivation, heterologous expression and feeding experiments, we fully explain the biosynthesis pathway of ophiobolin K in *Aspergillus ustus* 094102, especially proved to be an unclustered oxidase $OblC_{Au}$ that catalyzes dehydrogenation at the site of C16 and C17 of both ophiobolin F and ophiobolin C. We also find that the intermediate ophiobolin C and final product ophiobolin K could be transported into a space between the cell wall and membrane by $OblD_{Au}$ to avoid the inhibiting of cell growth, which is proved by a fluorescence observation of the subcellular localization and cytotoxicity tests. This study completely resolves the biosynthesis mechanism of ophiobolins in strain *A. ustus* 094102. At the same time, it is revealed that the burden of strain growth caused by the excessive accumulation and toxicity of secondary metabolites is closely related to

4.1. General Experiential Materials

DNA fragments for construction of plasmids were amplified using I-5™ 2×High-Fidelity Master Mix (TSINGKE Biotech, Beijing, China), whereas PCR for screening of transformants was performed using 2×Es Taq MasterMix (CWBIO, Beijing, China). Primers were synthesized by TSINGKE Biotech (Beijing, China) and sequencing was carried out in TSINGKE Biotech (Beijing, China). The 1 kb ladder (GDSBio, Guangzhou, China) was used as DNA marker. All restriction endonucleases were purchased from New England BioLabs (NEB; Ipswich, MA, USA). T-Vector pMD19 (Simple) was purchased from TaKaRa (Kyoto, Japan). ClonExpress Ultra One Step Clone Kit (Vazyme, Nanjing, China) was used for construction of plasmids rapidly.

The Biosynthesis and Transport of Ophiobolins in Aspergillus ustus 094102.
International Journal of Molecular Sciences. (IF: 6.21)

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Antibiotics (Basel). 2022 Sep 14;11(9):1246. doi: 10.3390/antibiotics11091246.

Molecular Characterization of Extended Spectrum β-Lactamase (ESBL) and Virulence Gene-Factors in Uropathogenic *Escherichia coli* (UPEC) in Children in Duhok City, Kurdistan Region, Iraq

Salwa Muhsin Hasan [1], Khalid S Ibrahim [2]

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PMID: 36140025 PMCID: PMC9495206 DOI: 10.3390/antibiotics11091246

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Abstract

Background: The presence of extended-spectrum β-lactamase (ESBL)-producing bacteria among uropathogens is significantly increasing in children all over the world. Thus, this research was conducted to investigate the prevalence of E. coli and their antimicrobial susceptibility pattern, and both genes of ESBL-producing E. coli resistant and virulence factor in UTIs patients among children in Duhok Province, Kurdistan, Iraq. Method: a total of 67 E. coli were identified from 260 urine samples of pediatric patients diagnosed with UTIs aged (0–15 years) which were collected from Heevi Pediatric Teaching Hospital, from August 2021 to the end of February 2022. Result: a high proportion of UPEC infections at ages <5 years and the rates among girls (88%) were significantly higher than those among the boys. A wide variety of E. coli are resistant to most antibiotics, such as Amoxicillin, Ampicillin and Tetracycline, and 64% of them were positive for ESBL. Interestingly, the presence of

Figure 1. Gel electrophoresis of PCR products for *E. coli*-specific primers *uidA* (**a**) marker genes (bla_{TEM}, bla_{CTX-M}, and bla_{SHV}) (**b–d**) and five virulence factors marker genes (*pai*, *hly*, *cnf-1*, *sfa* and *afa*) (**c–f**). The amplified DNA fragments produce of various *E. coli* strains with these marker primers: species-specific primer *uidA* (lanes 1–5 for strains 1–5) (**a**), CTX-M (lanes 1, 2 and 3 for control negative and strains 4 and 36, respectively) (**b**), TEM (lanes 1 and 2 for strains 4 and 36), *hly* (lanes 3 and 4 for strains 3 and 4 and lane 5 for control negative), and *sfa* (lanes 7 and 8, for strains 3 and 4) (**c**), SHV (lanes 1 and 2, for strains control positive and S36), *afa* (lanes 3 and 4, for strains 2 and 3) (**d**), *cnf-1* (lanes 1, 2, 3, 4, 5 and 6 for strains 4, 5, 6, 7, 8 and control-ve) (**e**), and *pai* (lanes 1, 2, and 3, for strains 4, 6 and 7) (**f**), and lane 100 bp Ladder (GDSBio Marker) (**b–e**) and 300 bp (GeneDireX, Marker) as shown in (**a**,**f**). A 7 µL of the PCR products and ladder were pipetted into a prepared 1.5% agarose gel stained with 5 µL of Safe Gel Stain Dye. Key: *pai*; pathogenicity island; *hly*; hemolysin, *sfa*; S-fimbrial adhesion, *cnf-1*; cytotoxic necrotizing factor-1, and *afa*; a fimbrial adhesion and S = strain.

Molecular Characterization of Extended Spectrum β-Lactamase (ESBL) and Virulence Gene-Factors in Uropathogenic Escherichia coli (UPEC) in Children in Duhok City, Kurdistan Region, Iraq.
Antibiotics-Basel. (IF: 5.22)

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Aquaculture
Volume 565, 25 February 2023, 739147

Screening and characterization of sex-specific markers by NGS sequencing in *Spinibarbus hollandi* with implication of XY sex determination system

Chong Han, Wenwei Huang, Suhan Peng, Jiangwei Zhou, Huawei Zhan, Lin Gui, Wenjun Li, Qiang Li

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Abstract

Sex-specific markers are critical for understanding sex determination mechanism and development of unisexual breeding in fish. *Spinibarbus hollandi* is an important commercial aquaculture species in southeastern China. Here, through whole genome

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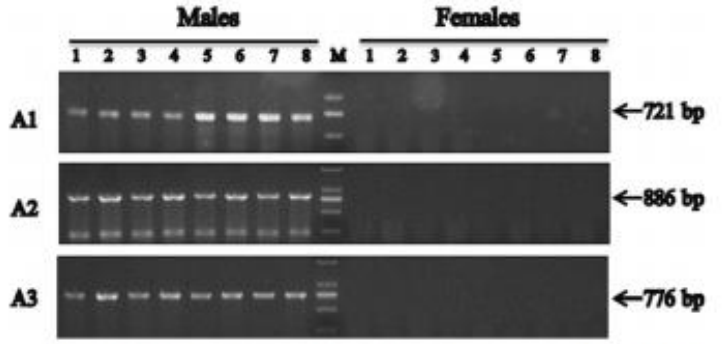

Fig. 1. The PCR detection and genetic sexing of three male-specific primers in eight females and eight males of *S. hollandi*. The DL 2000 DNA marker (GDSbio, China) is shown in the middle.

Screening and characterization of sex-specific markers by NGS sequencing in Spinibarbus hollandi with implication of XY sex determination system.
Aquaculture. (IF: 5.14)

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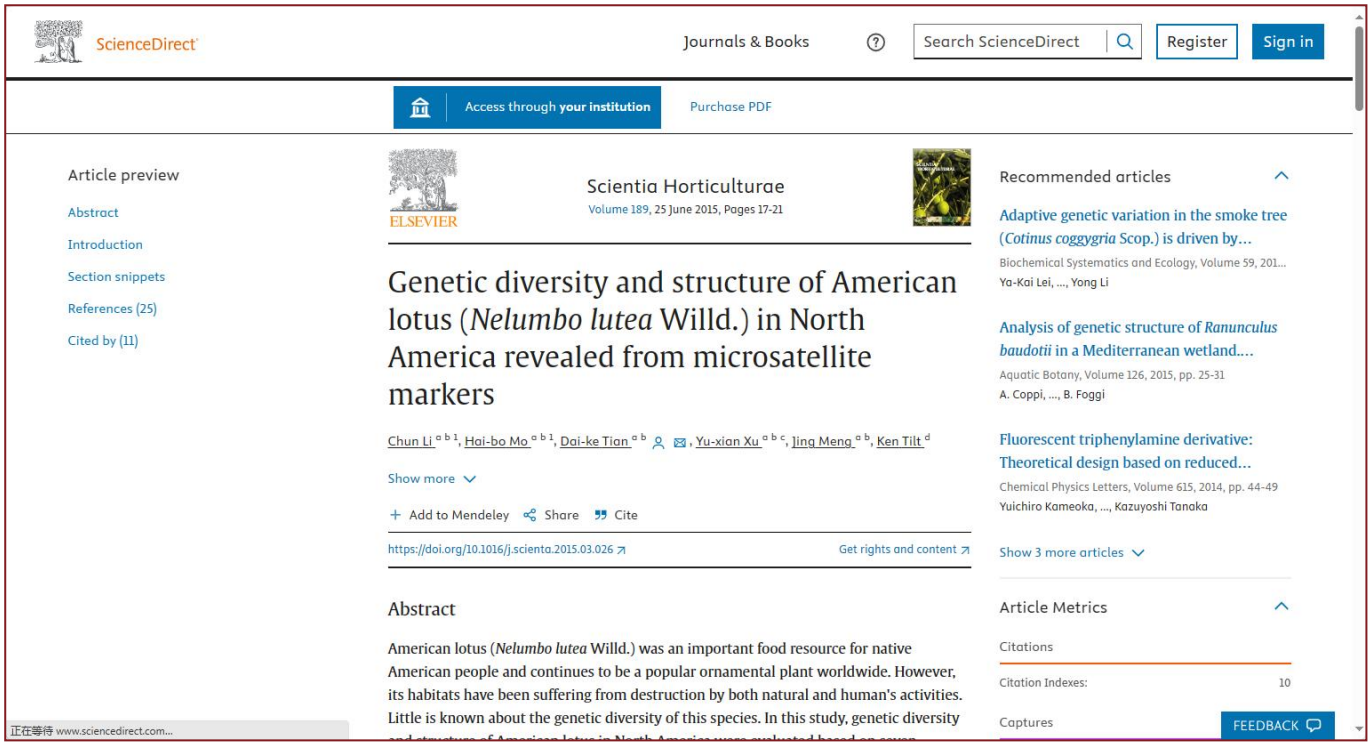

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Scientia Horticulturae
Volume 189, 25 June 2015, Pages 17-21

Genetic diversity and structure of American lotus (*Nelumbo lutea* Willd.) in North America revealed from microsatellite markers

Chun Li [a b 1], Hai-bo Mo [a b 1], Dai-ke Tian [a b], Yu-xian Xu [a b c], Jing Meng [a b], Ken Tilt [d]

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Abstract

American lotus (*Nelumbo lutea* Willd.) was an important food resource for native American people and continues to be a popular ornamental plant worldwide. However, its habitats have been suffering from destruction by both natural and human's activities. Little is known about the genetic diversity of this species. In this study, genetic diversity

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Genetic diversity and structure of American lotus (Nelumbo lutea Willd.) in North America revealed from microsatellite markers.
Scientia Horticulturae. (IF: 4.3)

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An asymmetric PCR-based, reliable and rapid single-tube native DNA engineering strategy

Yanzhen Bi, Xianfeng Qiao, Zaidong Hua, Liping Zhang, Ximei Liu, Li Li, Wenjun Hua, Hongwei Xiao, Jingrong Zhou, Qingxin Wei & Xinmin Zheng

BMC Biotechnology **12**, Article number: 39 (2012) | Cite this article

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Abstract

Background

Widely used restriction-dependent cloning methods are labour-intensive and time-consuming, while several types of ligase-independent cloning approaches have inherent limitations. A rapid and reliable method of cloning native DNA sequences into desired plasmids are highly desired.

Results

This paper introduces ABI-REC, a novel strategy combining asymmetric bridge PCR with

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Enzymes and reagents

ApaI, SalI, DpnI, BglII and XbaI restriction nucleases, *Taq* DNA polymerase and dNTP were purchased from Fermentas (Lithuania). KOD Plus high-fidelity DNA polymerase was purchased from Toyobo (Japan). A 1kb DNA ladder was from Dongsheng Co. Ltd. (Guangzhou, China). Enzymatic reactions were carried out under recommended conditions. All other chemicals used in the study were of molecular biology grade.

An asymmetric PCR-based, reliable and rapid single-tube native DNA engineering strategy.
BMC Biotechnology. (IF: 3.50)

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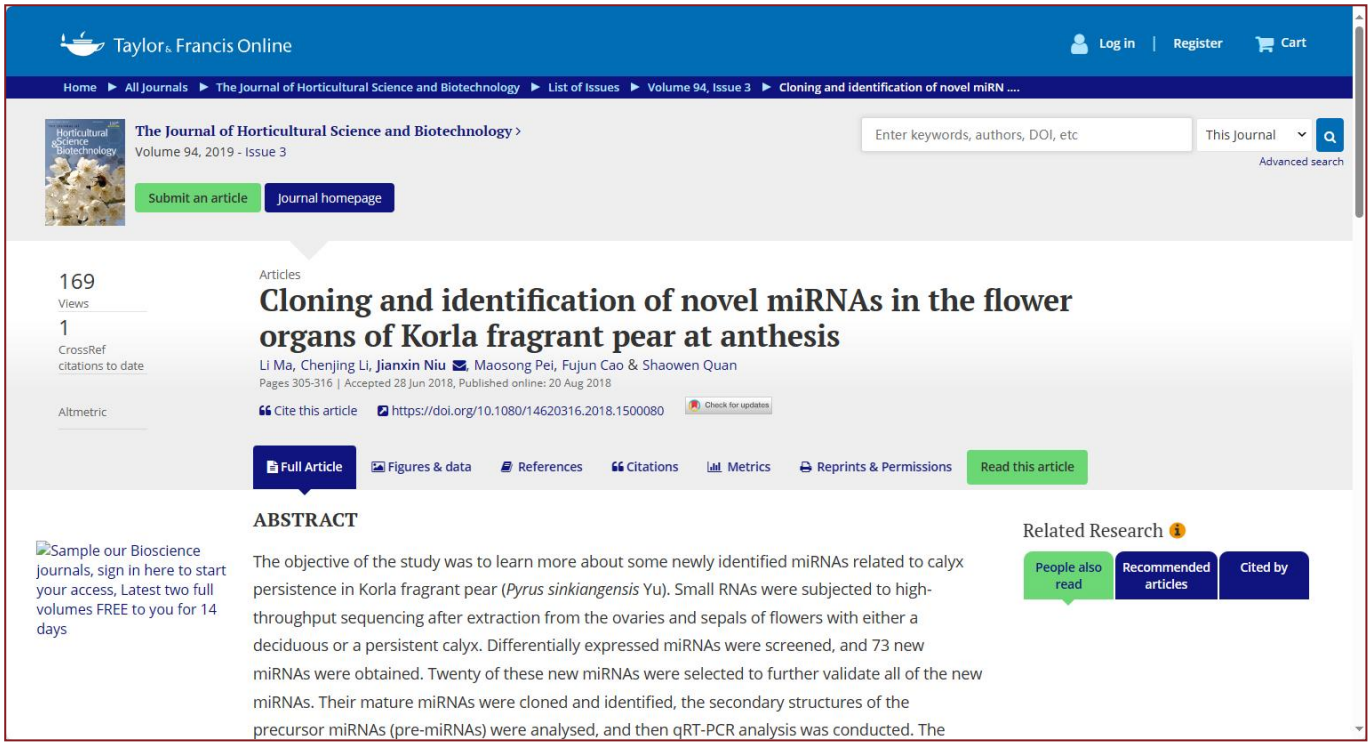

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Li Ma, Chenjing Li, **Jianxin Niu**, Maosong Pei, Fujun Cao & Shaowen Quan

Pages 305-316 | Accepted 28 Jun 2018, Published online: 20 Aug 2018

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ABSTRACT

The objective of the study was to learn more about some newly identified miRNAs related to calyx persistence in Korla fragrant pear (*Pyrus sinkiangensis* Yu). Small RNAs were subjected to high-throughput sequencing after extraction from the ovaries and sepals of flowers with either a deciduous or a persistent calyx. Differentially expressed miRNAs were screened, and 73 new miRNAs were obtained. Twenty of these new miRNAs were selected to further validate all of the new miRNAs. Their mature miRNAs were cloned and identified, the secondary structures of the precursor miRNAs (pre-miRNAs) were analysed, and then qRT-PCR analysis was conducted. The

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purchased from Tiangen Co (Beijing, China). The 20-bp ladder was purchased from Dongsheng Bio-tech Inc. (Guangzhou, China).

Cloning and identification of novel miRNAs in the flower organs of Korla fragrant pear at anthesis. Journal of horticultural science & biotechnology. (IF: 1.92)