

# **Qingxiang Guo, Ph.D.**

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**Postdoctoral Scholar, Feinberg School of Medicine, Northwestern University**

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Google Scholar: <https://scholar.google.com/citations?user=plx0LukAAAAJ&hl=en&oi=ao>

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## **I. Education**

**Ph.D**, Huazhong Agricultural University, Wuhan, Hubei, China (2014-2021)

**B.S**, Huazhong Agricultural University, Wuhan, Hubei, China (2010-2014)

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## **II. Research Interests & Expertise**

Cancer genomics and structural variant analysis; long-read RNA sequencing technologies; single-cell genomics and transcriptomics; deep learning applications in genomic data quality control; computational neoantigen discovery and immunogenomics; multi-omics data integration approaches; evolutionary and comparative genomics of early animals; host-pathogen interactions; phylogenetics/phylogenomics and molecular clocks; proteomic analysis of non-model organisms; integrative taxonomic systems and cross-species pathogen interactions

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## **III. Professional Appointments**

**Postdoctoral Scholar**, Northwestern University, Chicago, IL, USA (2022-Present)

- Developing computational approaches for cancer genomics under Dr. Rendong Yang's mentorship
- Creating tools for long-read sequencing and structural variant analysis
- Investigating anti-androgen resistance mechanisms in prostate cancer

**Graduate Research Assistant**, Huazhong Agricultural University, Wuhan, Hubei, China (2014-2021)

*Full-time research position during Ph.D. training, funded by institutional and external grants*

- Studied the phylogenetic status and divergence time of myxozoans using phylogenomics
- Investigated the phenotypic, environmental, and genetic adaptation mechanisms of myxozoans using multi-omics approaches

**International Intern**, Oregon State University, Corvallis, OR, USA (2014)

- Worked on evolutionary genomic and transcriptomic projects of myxozoans under Dr. Jerri Bartholomew
- Investigated cryptic life cycles of myxozoans

- Applied molecular techniques to understand host-parasite interactions

**Research Assistant**, Huazhong Agricultural University, Wuhan, Hubei, China (2011-2012)

- Studied distribution patterns of stromal eosinophil cells with Dr. Huazhen Liu
- Applied histological and immunohistochemical techniques

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## IV. Research Contributions

### 1. Integrated Multi-platform Structural Variant Analysis Toolkit

Developed **OctopuSV**, a comprehensive structural variant (SV) toolkit for multi-sample, cross-platform SV comparison and visualization. OctopuSV significantly improves accuracy in complex SV merging and breakpoint resolution across diverse genomic tools and sequencing technologies. The framework includes breakpoint (BND) correction algorithms, hierarchical SV classification systems, and automated visualization/reporting modules for enhanced interpretation. **TentacleSV** builds on OctopuSV to enable Snakemake-based large-scale SV benchmarking pipelines. These complementary tools have been successfully applied in prostate cancer genomics and single-cell datasets, revealing previously undetectable structural aberrations in cancer genomes.

Key publication: **Guo Q, Li Y, Wang TY, Ramakrishnan A, Yang R.** OctopuSV and TentacleSV: a one-stop toolkit for multi-sample, cross-platform structural variant comparison and analysis. *Bioinformatics*. 2025 Nov;41(11):btaf599.

### 2. Deep Learning for Detecting Chimeric Artifacts in Single-Cell Sequencing

Developed **ChimeraLM**, a deep learning classifier for detecting chimeric reads introduced by Multiple displacement amplification (MDA) amplification in single-cell long-read sequencing. We curated labeled datasets from dirty/clean data comparisons and built sequence-based classifiers. A **Mamba-based architecture** was implemented, enabling efficient detection of inversion-supporting chimera reads, with high precision and recall. Ongoing work includes cross-validation on independent datasets and model generalization to other SV types.

Key publication: - Manuscript in preparation.

### 3. Integrated Computational Pipeline for Multi-faceted Neoantigen Detection

Developed **ScanNeo2**, a comprehensive bioinformatics pipeline for *in silico* neoantigen discovery from diverse genomic and transcriptomic alterations. Traditional approaches often focus on single-nucleotide variants, overlooking additional sources such as gene fusions and alternative splicing. ScanNeo2 integrates multiple variant classes—canonical and exitron splicing, gene fusions, SNVs, indels—into a unified SnakeMake-based workflow, expanding the landscape of potentially immunogenic tumor-specific epitopes. The tool has been validated to accurately recapitulate experimentally confirmed immunogenic peptides, facilitating broader cancer immunotherapy research.

Key publication: - Schäfer RA, **Guo Q**, Yang R. ScanNeo2: a comprehensive workflow for neoantigen detection and immunogenicity prediction from diverse genomic and transcriptomic alterations. *Bioinformatics*. 2023 Nov;39(11):btad659.

#### 4. Evolutionary Genomics and Proteomics of Parasitic Cnidarians

Established a new paradigm in parasite evolution through comprehensive genomic and proteomic analyses of **myxozoans** (parasitic cnidarians). Discovered "mosaic evolution" in the *Myxobolus honghuensis* genome, challenging traditional views of parasite evolution as purely reductive by demonstrating significant innovation in multi-copy effector gene families alongside genomic simplification. Developed specialized methods for isolating nematocysts (specialized secretory organelles) using gradient ultracentrifugation techniques, and created the Comprehensive Proteomic Reference Database (CCPRD) to enable comparative analysis across species. This integrated approach revealed unique evolutionary patterns, species-specific protein adaptations, and an evolutionary lag between cellular structures and whole organisms, providing novel insights into how parasites adapt to specialized niches through balanced genomic expansion and reduction.

Key publications: **Guo Q**, Atkinson SD, Xiao B, Zhai Y, Bartholomew JL, Gu Z. A myxozoan genome reveals mosaic evolution in a parasitic cnidarian. *BMC Biol*. 2022 Feb 18;20(1):51. - Xiao B, **Guo Q**, Zhai Y, Gu Z. Transcriptomic Insights into the Diversity and Evolution of Myxozoa (Cnidaria, Endocnidozoa) Toxin-like Proteins. *Mar Drugs*. 2022 Apr 26;20(5). **Guo Q**, Whipps CM, Zhai Y, Li D, Gu Z. Quantitative Insights into the Contribution of Nematocysts to the Adaptive Success of Cnidarians Based on Proteomic Analysis. *Biology (Basel)*. 2022 Jan 7;11(1). - **Guo Q**, Li D, Zhai Y, Gu Z. CCPRD: A Novel Analytical Framework for the Comprehensive Proteomic Reference Database Construction of NonModel Organisms. *ACS Omega*. 2020 Jun 30;5(25):15370-15384. - **Guo Q**, Liu Y, Zhai Y, Gu Z. A fast and effective method for dissecting parasitic spores: myxozoans as an example. *J Exp Biol*. 2020 Jan 1.

#### 5. Integrative Taxonomic Systems and Host-Pathogen Interaction Networks

Developed a multidisciplinary framework for understanding myxozoan biology through integrated taxonomy and host-pathogen interaction studies. Created the "Counter-Evidence Response Strategy" to resolve conflicting morphological and molecular classifications in aquatic parasites, significantly advancing taxonomic standards across genera. Systematically investigated host-parasite relationships through developmental patterns and tissue tropism, documenting novel infection mechanisms including potential vertical transmission and organ-specific targeting. Conducted pioneering pathogenicity studies in mammalian models, establishing safety parameters for handling aquatic products. This work provided comprehensive insights into myxozoan life cycles and resolved longstanding taxonomic disputes, creating a unified understanding of parasite evolution, classification, and host interaction with applications in aquaculture disease management and food safety.

Key publications: Zhang B, **Guo Q**, Tu X, Gu Z. Identification of *Myxobolus distalisensis* n. sp. (Cnidaria: Myxozoa) infecting yellow catfish *Tachysurus fulvidraco* (Richardson), with a supplement description of *M. voremkhai* (Akhmerov, 1960) Landsberg and Lom, 1991. *Syst Parasitol*. 2023 Oct;100(5):473-485. - Zhang X, Liu Y, Whipps CM, **Guo Q**, Gu Z. Multiple evolutionary routes of the

single polar capsule in *Thelohanellus* species (Myxozoa; Myxobolidae). *Int J Parasitol Parasites Wildl*. 2019 Apr;8:56-62. - **Guo Q**, Huang M, Liu Y, Zhang X, Gu Z. Morphological plasticity in *Myxobolus* Bütschli, 1882: a taxonomic dilemma case and renaming of a parasite species of the common carp. *Parasit Vectors*. 2018 Jul 9;11(1):399. Wang S, Zhang B, **Guo Q**, Zhai Y, Gu Z. Molecular and light microscopy evidence for the transfer of *Myxobolus honghuensis* from *Carassius auratus gibelio* broodfish to progeny. *J Fish Dis*. 2020 Oct;43(10):1177-1184. - **Guo Q**, Zhai Y, Gu Z, Liu Y. Histopathological and ultrastructural studies of *Myxobolus turpisrotundus* from allogynogenetic gibel carp *Carassius auratus gibelio* in China. *Folia Parasitol (Praha)*. 2016 Oct 14;63. - **Guo Q**, Jia L, Qin J, Li H, Gu Z. Myxozoans and Our Dinner Table: Pathogenicity Studies of *Myxobolus honghuensis* (Myxosporea: Bivalvulida) Using a Suckling Mice Model. *Foodborne Pathog Dis*. 2015 Aug;12(8):653-60.

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## V. Publications

### Peer-Reviewed Journal Articles

#### (Co)-First-author Publications

1. **Guo Q**, Li Y, Wang TY, Ramakrishnan A, Yang R. OctopusV and TentacleSV: a one-stop toolkit for multi-sample, cross-platform structural variant comparison and analysis. *Bioinformatics*. 2025 Nov;41(11):btaf599.
2. **Guo Q**, Atkinson SD, Xiao B, Zhai Y, Bartholomew JL, Gu Z. A myxozoan genome reveals mosaic evolution in a parasitic cnidarian. *BMC Biol*. 2022 Feb 18;20(1):51.
3. **Guo Q**, Whipps CM, Zhai Y, Li D, Gu Z. Quantitative insights into the contribution of nematocysts to the adaptive success of cnidarians based on proteomic analysis. *Biology (Basel)*. 2022 Jan 7;11(1).
4. **Guo Q**, Liu Y, Zhai Y, Gu Z. A fast and effective method for dissecting parasitic spores: myxozoans as an example. *J Exp Biol*. 2020 Jan 1;223(10):jeb214916.
5. **Guo Q**, Li D, Zhai Y, Gu Z. CCPRD: A novel analytical framework for the comprehensive proteomic reference database construction of nonmodel organisms. *ACS Omega*. 2020 Jun 30;5(25):15370-15384.
6. **Guo Q**, Huang M, Liu Y, Zhang X, Gu Z. Morphological plasticity in *Myxobolus* Bütschli, 1882: a taxonomic dilemma case and renaming of a parasite species of the common carp. *Parasit Vectors*. 2018 Jul 9;11(1):399.
7. **Guo Q**, Zhai Y, Gu Z, Liu Y. Histopathological and ultrastructural studies of *Myxobolus turpisrotundus* from allogynogenetic gibel carp *Carassius auratus gibelio* in China. *Folia Parasitol (Praha)*. 2016 Oct 14;63.
8. **Guo Q**, Jia L, Qin J, Li H, Gu Z. Myxozoans and our dinner table: pathogenicity studies of *Myxobolus honghuensis* (Myxosporea: Bivalvulida) using a suckling mice model. *Foodborne Pathog Dis*. 2015 Aug;12(8):653-60.

#### Co-authored Publications

8. Yang Y, Wang TY, Li Q, Lu J, Ren Y, Weiner AB, Fry J, Liu Q, Yum C, Wang R, **Guo Q**, Wan Y, Zhe J, Dong X, Lotan TL, Schaeffer EM, Yang R, Cao Q. Androgen receptor-regulated

lncRNA PRCAT71 promotes AR signaling through the interaction with KHSRP in prostate cancer. *Sci Adv.* 2025 Apr;11(15):eadk6989.

9. Schäfer RA, **Guo Q**, Yang R. ScanNeo2: a comprehensive workflow for neoantigen detection and immunogenicity prediction from diverse genomic and transcriptomic alterations. *Bioinformatics.* 2023 Nov;39(11):btad659.
10. Zhang B, **Guo Q**, Tu X, Gu Z. Identification of *Myxobolus distalisensis* n. sp. (Cnidaria: Myxozoa) infecting yellow catfish *Tachysurus fulvidraco* (Richardson), with a supplement description of *M. voremkhai* (Akhmerov, 1960) Landsberg and Lom, 1991. *Syst Parasitol.* 2023 Oct;100(5):473-485.
11. Xiao B, **Guo Q**, Zhai Y, Gu Z. Transcriptomic insights into the diversity and evolution of Myxozoa (Cnidaria, Endocnidozoa) toxin-like proteins. *Mar Drugs.* 2022 Apr 26;20(5).
12. Tahir UB, **Guo Q**, Gu Z. Fins infestation induced by *Myxobolus xiantaoensis* in yellow catfish *Tachysurus fulvidraco* Richardson, 1846: Some pathophysiological and molecular insights. *Microb Pathog.* 2021 Apr;153:104772.
13. Wang S, Zhang B, **Guo Q**, Zhai Y, Gu Z. Molecular and light microscopy evidence for the transfer of *Myxobolus honghuensis* from *Carassius auratus gibelio* broodfish to progeny. *J Fish Dis.* 2020 Oct;43(10):1177-1184.
14. Zhang X, Liu Y, Whipps CM, **Guo Q**, Gu Z. Multiple evolutionary routes of the single polar capsule in *Thelohanellus* species (Myxozoa; Myxobolidae). *Int J Parasitol Parasites Wildl.* 2019 Apr;8:56-62.
15. Tahir UB, **Guo Q**, Zhao D, Liu Y, Gu Z. Description of *Myxobolus xiantaoensis* n. sp. from the fins of yellow catfish in China: a species previously attributed to *Myxobolus physophilus* Reuss, 1906 in Chinese records. *Parasitol Res.* 2019 Apr;118(4):1137-1146.
16. Shao J, **Guo Q**, Hu R, Gu Z. Comparative genomic insights into the taxonomy of *Edwardsiella tarda* isolated from different hosts: marine, freshwater and migratory fish. *Aquaculture Research.* 2018 January;49(1):197-204.
17. Wang Z, Zhou T, **Guo Q**, Gu Z. Description of a new freshwater ciliate *Epistylis wuhanensis* n. sp. (Ciliophora, Peritrichia) from China, with a focus on phylogenetic relationships within family Epistylididae. *Journal of Eukaryotic Microbiology.* 2017;64(3):394-406.
18. Liu Y, **Guo Q**, Zhai Y, Gu Z. Effects of different preservation methods on morphology of *Myxobolus wulii* spores. *Journal of Huazhong Agricultural University.* 2016;(4):87-92. (In Chinese with English abstract)
19. Zhai Y, Gu Z, **Guo Q**, Wu Z, Wang H, Liu Y. New type of pathogenicity of *Thelohanellus kitaeui* Egusa & Nakajima, 1981 infecting the skin of common carp *Cyprinus carpio* L. *Parasitol Int.* 2016 Feb;65(1):78-82.
20. Zhai Y, Whipps CM, Gu Z, **Guo Q**, Wu Z, Wang H, Liu Y. Intraspecific morphometric variation in myxosporeans. *Folia Parasitol (Praha).* 2016 Apr 1;63.
21. Deng Q, **Guo Q**, Zhai Y, Wang Z, Gu Z. First record of *Chilodonella piscicola* (Ciliophora: Chilodonellidae) from two endangered fishes, *Schizothorax o'connori* and *Oxygymnocypris stewartii* in Tibet. *Parasitol Res.* 2015 Apr;114(8):3097-3103.

22. Jia L, Gu Z, Liu Y, **Guo Q**, Li D, Zhai Y. Preparation and characterization of polyclonal antibodies against *Myxobolus honghuensis* (Myxosporea: Bivalvulida). *Journal of Huazhong Agricultural University*. 2015;(6):113-118. (In Chinese with English abstract)
23. Zhang JY, Gu ZM, Kalavati C, Costa Eiras J, Liu Y, **Guo Q**, Molnár K. Synopsis of the species of *Thelohanellus* Kudo, 1933 (Myxozoa: Myxosporea: Bivalvulida). *Syst Parasitol*. 2013 Nov;86(3):235-56.

## Manuscripts in Preparation/Submitted

1. Li Y, Wang TY, **Guo Q**, Ren Y, Lu X, Cao Q, Yang R. A genomic language model for chimera artifact detection in nanopore direct RNA sequencing. *Nature Communications* (Revision). 2025.
2. Yang Y, Wang TY, Fry J, Li Y, Meng Q, **Guo Q**, Patchen N, Ramakrishnan A, Ren Y, Dawes C, Fragkogianni M, Irvin P, Zhang X, Alam SK, Hoeppner L, Zhang X, Yee D, Weiner A, Schaeffer E, Liu Y, Dehm S, Cao Q. Tumor-specific lncRNA IGF1R-AS1 trans-regulates chromatin interactions associated with oncogenic MYC signaling. *Nature Communications* (Revision). 2025.

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## VI. Patents

1. Gu Z, **Guo Q**, Zhai Y, Liu Y. A method to isolate and purify the nematocyst of *Myxobolus honghuensis* (Myxosporea: Bivalvulida). China Patent Application No. CN110055181B. 2022.
2. Gu Z, Li D, Liu Y, **Guo Q**. A PCR method for simultaneous detection of multiple myxozoans in allogynogenetic gibel carp *Carassius auratus gibelio*. China Patent No. ZL201610051386.8. 2019.
3. Gu Z, Jia L, Liu Y, Zhai Y, Yuan J, Qin J, Li D, **Guo Q**. Preparation and application of polyclonal antibodies against the shell valves of *Myxobolus honghuensis* (Myxosporea: Bivalvulida). China Patent No. CN103755806B. 2016.
4. Gu Z, Jia L, Liu Y, Zhai Y, Yuan J, Qin J, Li D, **Guo Q**. Preparation and application of polyclonal antibodies against the polar filaments of *Myxobolus honghuensis* (Myxosporea: Bivalvulida). China Patent No. CN103880954B. 2015.
5. Gu Z, **Guo Q**, Zhai Y, Liu Y. A method to isolate and purify the shell valves of *Myxobolus wulii* (Myxosporea: Bivalvulida). China Patent Application No. ZL CN110004104B. 2022

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## VII. Presentations

### Oral Presentations

1. Morphological plasticity in *Myxobolus*: a taxonomic dilemma case. The 3rd Chinese Protozoological Society Scholars Symposium, Jilin, China (2018)
2. Lights into the evolutionary scenario of extrusion apparatus in eukaryotes. The 19th Symposium of Chinese Protozoological Society, Sun Yat-sen University, China (2017)

3. Histopathological and ultrastructural studies of *Myxobolus turpisrotundus*. The 2nd Chinese Protozoological Society Scholars Symposium, Shanghai, China (2016)
4. Pathogenicity studies of *Myxobolus* using a suckling mice model. The 7th International Symposium on Aquatic Animal Health, Portland, USA (2014)
5. Pathogenicity studies of *Myxobolus* using a suckling mice model. The 17th Symposium of Chinese Protozoological Society, Jilin University, China (2013)

## Poster Presentations

1. Lights into the evolutionary scenario of extrusion apparatus in eukaryotes. The annual meeting of the Society for Molecular Biology and Evolution, Austin, USA (2017)
2. Comparative transcriptomic insights into the origin and evolution of myxozoans. The 3rd National Academic Summit on Functional Genomics, Beijing, China (2016)
3. Comparative transcriptomic insights into the origin and evolution of myxozoans. The 18th Symposium of Chinese Protozoological Society, Yantai, China (2015)

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## VIII. Honors and Awards

1. Second Prize, Simulated International Academic Conference of Postgraduate Students (2016)
  - Only two prize winners in Huazhong Agricultural University this year
2. The Best Presenter Award, Academic Annual Meeting of College of Fisheries, Huazhong Agricultural University (2015)
3. Champion Award, The First Frasergen Bioinformatics Contest (2014)
  - Only one prize winner out of the 150 contestants from universities in China
4. The Outstanding Individual, The Professional Social Practice Competition in Hubei Province (2012)
  - Awarded for the best team leader in professional practice; only 415 winners in China this year

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## IX. Teaching and Mentoring Experience

**Teaching Assistant**, Fish Diseases course, Huazhong Agricultural University (2015)

- Led section discussions for 31 students
- Prepared laboratory reagents
- Wrote and graded exams

### **Undergraduate Mentor, Fisheries, Huazhong Agricultural University (2012-2013)**

- Provided social support, professional development, and career guidance to 35 first-year students

### **Supervisor, Huazhong Agricultural University (2015-2018)**

- Direct supervisor of seven undergraduates on their senior theses

### **Research Mentor, Northwestern University (2023)**

- Mentored Timothy Pan, PhD student (Driskill Graduate Program), during laboratory rotation
- Provided guidance in experimental design, data analysis, and lab workflows

### **Research Mentor, Northwestern University (2024)**

- Supervised Alice Kong, high school student (Payton College Preparatory High School), ResearchSTAR Summer Intern
- Introduced core research concepts, laboratory techniques, and scientific thinking

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## X. Professional Service

### Manuscript Review

Served as reviewer for: Cancers (6), International Journal of Molecular Sciences (4), Foodborne Pathogens and Disease (4), Computational and Structural Biotechnology Journal (3), Biology (2), Biomedicines (1), BMC Genomics (2), BMC Biology (1), BMC Genomic Data (1), Cells (1), Diversity (1), Genes (1), Journal of Clinical Medicine (1), Journal of Marine Science and Engineering (1), Scientific Reports (1), Translational Oncology (1), Antibodies (1), Journal of Imaging (2), Frontiers in bioinformatics (1), Antioxidants (1).

### Professional Memberships

- Society for Molecular Biology and Evolution (2017-Present)
- China Society of Fisheries (2015-2020)
- Chinese Protozoological Society (2013-2020)

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## XI. Technical Skills

### Bioinformatics and Omics Analysis

- Long-read sequencing (ONT, PacBio) and analysis
- Structural variant detection, annotation and interpretation
- Genome assembly, annotation and comparative genomics

- Transcriptomics: RNA-protein interactions, splicing analysis, lncRNA identification
- Single-cell genomics: MDA artifact detection, variant calling, multi-omics integration
- Single-cell RNA-seq: Quality control, normalization, cell-type identification
- Proteomics: Mass spectrometry analysis, database construction (CCPRD)

## Computational Skills

- Languages: Python, R, Bash/Shell, Perl, SQL
- Workflow management (Snakemake) and version control (Git)
- Deep learning: CNN, Mamba architectures
- Phylogenomics: OrthoMCL, RAxML, IQ-TREE, PhyloBayes
- Evolutionary analysis: BEAST, R8S, HYPHY, PAML

## Laboratory Skills

- ONT long-read sequencing library preparation
- Molecular biology techniques (PCR, Western blot, cloning)
- Animal handling (mice, fish)
- Histological techniques
- Microscopy (light, fluorescence, TEM)