Objective 1: Advance the status of reference genomes for all species, including basic annotation of worldwide genetic variation, by broad sequencing among different lines and breeds of animals.

We have sequenced, assembled and annotated the YY genome of channel catfish using a YY sequencing template that avoid any X chromosome sequences in the assembly. The YY genome sequence assembly is of high quality with a contig N50 size of 2.7 Mb and a scaffold N50 size of 26.7 Mb. The genome assembly is validated through linkage mapping of more than 250,000 SNP markers.

Objective 2: Develop strategies to identify and exploit genes and allelic variation that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.

We have identified a candidate for sex determination gene in catfish through positional and functional evidence. Genetic linkage and GWAS analyses placed the sex determination locus within a genetic distance less than 0.5 cM and physical distance of 8.9 Mb. However, comparison of the channel catfish X and Y chromosome sequences revealed no chromosome-specific genes. Comparative RNA-Seq analysis between females and males revealed exclusive sex-specific expression of a transcript isoform of the candidate gene. Experimental knockout of the candidate gene converted genetic males (XY) to phenotypic females, providing functional support of the candidate as the sex determination gene.

We have identified a series of QTLs controlling disease resistance for ESC, columnaris, head size, body conformation, tolerance to low oxygen, and growth. These works have been published.

Publications

1. Jin Y, Zhou T, Li N, Liu S, Xu X, Tan S, Shi H, Yang Y, Yuan Z, Wang W, Pan Y, Gao D, Dunham R, Liu ZJ. 2018. JAK and STAT members in channel catfish: Identification, phylogenetic analysis and expression profiling after bacterial infection. Developmental and Comparative Immunology, in press.
2. Yuan Z, Huang W, Liu S, Xu P, Dunham R, Liu ZJ. 2018. Historical demography of common carp estimated from individuals collected from various parts of the world using the pairwise sequentially Markovian coalescent approach. Genetica, in press.
3. Yang Y, Fu Q, Liu Y, Wang X, Dunham R, Liu S, Bao L, Zeng Q, Zhou T, Li N, Qin Z, Jiang C, Gao D, Liu ZJ. 2018. Comparative transcriptome analysis reveals conserved branching morphogenesis related genes involved in chamber formation of catfish swimbladder. Physiological Genomics, in press.
4. Fu Q, Yang Y, Li C, Zeng Q, Zhou T, Li N, Liu Y, Liu S, Li D, Liu ZJ. 2017. The CC and CXC chemokine receptors in channel catfish (*Ictalurus punctatus*) and their involvement in disease and hypoxia responses. Developmental and Comparative Immunology 77: 241-251.
5. Fu Q, Yang Y, Li C, Zeng Q, Zhou T, Li N, Liu Y, Li Y, Wang X, Liu S, Li D, Liu ZJ. 2017. The chemokinome superfamily: II. The 64 CC chemokines in channel catfish and their involvement in disease and hypoxia responses. Developmental and Comparative Immunology 73: 97-108.
6. Geng X, Liu S, Yuan Z, Jiang Y, Zhi D, and Liu ZJ. 2017. A genome wide association study reveals that genes with functions for bone development are associated with body conformation in catfish. Marine Biotechnology 19: 570-578.
7. Wang X, Liu S, Dunham R, Liu ZJ. 2017. Effects of strain and body weight on low-oxygen tolerance of channel catfish. Aquaculture International 25: 1645-1652. DOI: 10.1007/s10499-017-0125-2
8. The Aquaculture Genomics, Genetics and Breeding Workshop, Abdelrahman H, ElHady M, Alcivar-Warren A, Allen S, Al-Tobasei R, Bao L, Beck B, Blackburn H, Bosworth B, Buchanan J, Chappell J, Daniels W, Dong S, Dunham R, Durland E, Elaswad A, Gomez-Chiarri M, Gosh K, Guo X, Hackett P, Hanson T, Hedgecock D, Howard T, Holland L, Jackson M, Jin Y, Kahlil K, Kocher T, Leeds T, Li N, Lindsey L, Liu S, Liu ZJ\*, Martin K, Novriadi R, Odin R, Palti Y, Peatman E, Proestou D, Qin G, Reading B, Rexroad C, Roberts S, Salem M, Severin A, Shi H, Shoemaker C, Stiles S, Tan S, Tang KFJ, Thongda W, Tiersch T, Tomasso J, Tri Prabowo W, Vallejo R, van der Steen H, Vo K, Waldbieser G, Wang H, Wang X, Xiang J, Yang Y, Yant R, Yuan Z, Zeng Q, and Zhou T. 2017. Aquaculture genomics, genetics and breeding in the United States: current status, challenges, and priorities for future research. BMC Genomics 18: 191. DOI 10.1186/s12864-017-3557-1
9. Wang X, Liu S, Yang Y, Fu Q, Abebe A, Liu ZJ. 2017. Identification of NF-κB related genes in channel catfish and their expression profiles in mucosal tissues after columnaris bacterial infection. Developmental and Comparative Immunology 70: 27-38.
10. Li N, Zhou T, Geng X, Jin Y, Wang X, Liu S, Xu X, Gao D, Li Q, **Liu ZJ.** 2017. Identification of novel genes significantly affecting growth in catfish through GWAS analysis. Molecular Genetics and Genomics, in press. doi.org/10.1007/s00438-017-1406-1
11. Yuan Z, Liu S, Bao L, Zhou T, Liu ZJ. 2017. Comparative genome analysis of 52 fish species suggests differential associations of repetitive elements with their living aquatic environments. BMC Genomics, in press.
12. Zhong X, Wang X, Zhou T, Jin Y, Tan S, Jiang C, Geng X, Li N, Shi H, Zeng Q, Yang Y, Yuan Z, Bao L, Tian C, Liu S, Li Q, **Liu ZJ.** 2017. Genome-wide association study reveals multiple novel QTL associated with low-oxygen tolerance in hybrid catfish. Marine Biotechnology 19: 379-390. DOI: 10.1007/s10126-017-9757-5.
13. Li Y, Geng X, Bao L, Elaswad A, Huggins KW, Dunham R, Liu ZJ. 2017. A deletion in the Hermansky-Pudlak syndrome 4 (Hps4) gene appears to be responsible for albinism in channel catfish. Molecular Genetics and Genomics, in press. DOI 10.1007/s00438-017-1302-8
14. Nunes, José de Ribamar da Silva, Liu S, Pértille F, Perazza C, Vera Maria Fonseca de Almeida Val, Hilsdorf AWS, Liu ZJ, & Coutinho LL. 2017. Large-scale SNP discovery and construction of a high-density genetic map of tambaqui (*Colossoma macropomum*) through genotyping-by-sequencing. Scientific Report 7: 46112.
15. Zhou T, Liu S, Geng X, Jin Y, Jiang C, Bao L, Yao J, Zhang Y, Zhang J, Sun L, Wang X, Li N, Tan S, Liu ZJ. 2017. GWAS analysis of QTL for enteric septicemia of catfish and their involved genes suggest evolutionary conservation of a molecular mechanism of disease resistance. Molecular Genetics and Genomics 292: 231-242. DOI 10.1007/s00438-016-1269-x
16. Gao S, and Liu ZJ. 2017. Taste receptors and gustatory associated G proteins in channel catfish, *Ictalurus punctatus*. Comparative Biochemistry and Physiology, part D, Genomics and Proteomics 21: 1-9. doi.org/10.1016/j.cbd.2016.10.002.
17. Gao S, Liu S, Yao J, Li N, Yuan Z, Zhou T, Li Q, and Liu ZJ. 2017. Genomic organization and evolution of olfactory receptors and trace amine-associated receptors in channel catfish, *Ictalurus punctatus*. Biochimica et Biophysica Acta - General Subjects 1861 (2017): 644-651. Doi 10.1016/j.bbagen.2016.10.017.
18. Zeng Q, Fu Q, Li Y, Waldbieser G, Bosworth B, Liu S, Yang Y, Bao L, Yuan Z, Li N, and Liu ZJ. 2017. Development of a 690K SNP array in catfish and its application for genetic mapping of 250,000 markers and validation of the reference genome sequence. Scientific Report 7: 40347 DOI:10.1038/srep40347.
19. Zhou T, Li N, Liu S, Jin Y, Fu Q, Gao S, Wang X, Liu ZJ. 2017. The NCK and ABI adaptor genes in catfish and their involvement in ESC disease responses. Developmental and Comparative Immunology 73: 119-123.
20. Tian C, Tan S, Bao L, Zeng Q, Liu S, Yang Y, Zhong X, Liu ZJ. 2017. DExD/H-box RNA helicase genes are differentially expressed between males and females during the critical period of male sex differentiation in channel catfish. Comparative Biochemistry and Physiology part D 22: 109-119.
21. Fu Q, Zeng Q, Li Y, Yang Y, Li C, Zhou T, Li N, Liu S, Yao J, Jiang C, Li D, **Liu ZJ.** 2017. The chemokinome superfamily in channel catfish: I. CXC subfamily and their involvement in disease defense and hypoxia responses. Fish and Shellfish Immunology 60: 380-390.