

教育和工作经历

2017.09 – 至 今 : 四川大学, 生命科学学院, 副教授

2014.07 – 2017.09 : 四川大学, 生命科学学院, 特聘副研究员

2011.02 – 2014.01 : 美国加州大学洛杉矶分校, Robert Wayne教授实验室, 博士联合培养

2007.09 – 2014.07 : 四川大学, 生命科学学院, 获理学博士学位 (导师: 岳碧松教授)

研究方向

主要利用生物信息学方法对多组学数据 (基因组、普通转录组、单细胞转录组、甲基化组、宏基因组、代谢组等) 进行整合研究, 结合分子生物学技术和动物实验等手段, 开展如下研究:

1. 以西南地区的野生动物和青藏高原的特有动物为主要研究对象, 开展适应性演化、微生物和宿主协同进化等研究
2. 以猕猴等非人灵长类为研究对象, 开展腹泻、衰老机制等研究
3. 与医学院合作, 对阴道炎、儿童肥胖、血液安全等进行合作研究, 提供生物信息支持

学术兼职

- 中国动物学会灵长类学分会理事会第一届 (2017-2021) 和第二届理事 (2022-2026)
- 中国动物学会生物进化理论专业委员会第四届委员会委员 (2022-2026)
- 四川省动物学会理事 (2022-2027)

获奖及荣誉

- 2015 年度四川大学青年科技人才奖
- 2015 年四川省科技进步二等奖 (排名第六, 登记号: 9512015Y1603)
- 2018 年入选第十二批四川省学术和技术带头人后备人选

科研项目

1. 国家自然科学基金委员会, 面上项目, 32370450, 基于多组学技术研究肠道微生物在猕猴 (*Macaca mulatta*) 衰老过程中的作用机制, 2024 年 1 月至 2027 年 12 月, 主持
2. 国家自然科学基金委员会, 面上项目, 32070413, 猕猴 (*Macaca mulatta*) 衰老过程中凝血功能变化规律及基因表达调控机制研究, 2021 年 1 月至 2024 年 12 月, 主持
3. 国家自然科学基金委员会, 青年科学基金项目, 31501871, 基于血液转录组的藏酋猴免疫和糖代谢相关基因的表达研究, 2016 年 1 月至 2018 年 12 月, 主持
4. 四川省自然科学基金, 杰出青年科学基金项目, 2023NSFSC1935, 基于宏基因组学和培养组学的实验猕猴腹泻机制研究和新型微生态制剂的开发, 2023 年 1 月至 2025 年 12 月, 主持

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5. 四川省科技厅, 重点研发计划, 2023YFS0034, 儿童肥胖代谢性疾病精准防治研究, 2023年1月至2024年12月, 参与
6. 四川省科技厅, 应用基础, 2020YJ0303, 猕猴衰老过程基因表达变化及衰老模型初步研究, 2020年1月至2021年12月, 主持

2018年以来发表的SCI论文 (#第一作者, *通讯作者)

◆ 非人灵长类相关研究

1. Wang J[#], Liu X[#], Lan Y, Que T, Li J, Yue B, Fan Z*. DNA methylation and transcriptome analysis reveal epigenomic differences among three macaque species. *Evolutionary Applications*. 2024 Feb;17:e13604.
2. Wu J, Zhou Q, Qi H, Lan W, Yang S, Yang S, Fan Z*, Zhang A*. Antimicrobial resistance spectrum and virulence characterization of Escherichia coli, Klebsiella pneumoniae and Proteus mirabilis isolated from asymptomatic and diarrheal rhesus monkeys. *Microbiology Research*. 2024 Feb 1;282:127633.
3. Yang S[#], Fan Z[#], Li J, Wang X, Lan Y, Yue B, He M, Zhang A*, Li J*. Assembly of novel microbial genomes from gut metagenomes of rhesus macaque (*Macaca mulatta*). *Gut Microbes*. 2023 Jan-Dec;15(1):2188848. (大类一区TOP期刊 ; 5年平均IF = 12.4)
4. Liu X, Liu X, Wang X, Shang K, Li J, Lan Y, Wang J, Li J, Yue B, He M*, Fan Z*. Multi-omics analysis reveals changes in tryptophan and cholesterol metabolism before and after sexual maturation in captive macaques. *BMC Genomics*. 2023 Jun 7;24(1):308.
5. Yang S[#], Liu Y[#], Yang N[#], Lan Y, Lan W, Feng J, Yue B, He M, Zhang L, Zhang A, Price M, Li J*, Fan Z*. The gut microbiome and antibiotic resistome of chronic diarrhea rhesus macaques (*Macaca mulatta*) and its similarity to the human gut microbiome. *Microbiome*. 2022 Feb 9;10(1):29. (大类一区TOP期刊 ; 5年平均IF = 19.4)
6. Xu J[#], Lan Y[#], Wang X, Shang K, Liu X, Wang J, Li J, Yue B, Shao M*, Fan Z*. Multi-omics analysis reveals the host-microbe interactions in aged rhesus macaques. *Frontiers in Microbiology* 2022 Sep 27;13:993879.
7. Wang J[#], Lan Y[#], He L, Tang R, Li Y, Huang Y, Liang S, Gao Z, Price M, Yue B, He M, Guo T*, Fan Z*. Sex-specific gene expression in the blood of four primates. *Genomics*. 2021 Jul;113(4):2605-2613.
8. Wang J[#], Lv M[#], He L, Wang X, Lan Y, Chen J, Chen M, Zhang C, Tang R, Zhou D, Deng X, Li J, Guo T, Price M, Yue B, Fan Z*. Transcriptomic landscape of persistent diarrhoea in rhesus macaques and comparison with humans and mouse models with inflammatory bowel disease. *Gene*. 2021 Oct 20;800:145837.
9. Yan C[#], Zhang X[#], Zhou L, Yang Q, Zhou M, Zhang L, Xing J, Yan Z, Price M, Li J, Yue B, Fan Z*. Effects of aging on gene expression in blood of captive Tibetan macaques (*Macaca thibetana*) and comparisons with expression in humans. *Zoological Research* 2020 Sep 18;41(5):557-563. (大类一区)
10. Lan Y[#], Wang J[#], Yang Q, Tang R, Zhou M, Lei G, Li J, Zhang L, Yue B, Fan Z*. Blood transcriptome analysis reveals gene expression features of breast-feeding rhesus macaque (*Macaca mulatta*) infants. *Zoological Research* 2020 Jul 18;41(4):431-436. (大类一区)
11. Zhou M[#], Zhang L[#], Yang Q[#], Yan C, Jiang P, Lan Y, Wang J, Tang R, He M, Lei G, Sun P, Su N, Price M, Li J, Lin F, Yue B*, Fan Z*. Age-related gene expression and DNA methylation changes in rhesus macaque. *Genomics*. 2020 Nov;112(6):5147-5156.
12. Fan Z, Zhou A, Osada N, Yu J, Jiang J, Li P, Du L, Niu L, Deng J, Xu H, Xing J, Yue B*, Li J*. Ancient hybridization and admixture in macaques (genus *Macaca*) inferred from whole genome sequences. *Molecular Phylogenetics and Evolution* 2018 Oct;127:376-386. (大类一区 TOP 期刊)

◆ 野生动物相关研究

1. Tang R[#], Wang J[#], Li YF[#], Zhou C[#], Meng G, Li F, Lan Y, Price M, Podsiadlowski L, Yu Y, Wang X, Liu Y,

- Yue B, Liu S, **Fan Z***, Liu S*. Genomics and morphometrics reveal the adaptive evolution of pikas. *Zoological Research* 2022 Sep;43(5):813-826. (大类一区)
2. Lan Y#, He L#, Dong X, Tang R, Li W, Wang J, Wang L, Yue B, Price M, Guo T*, **Fan Z***. Comparative transcriptomes of three different skin sites for the Asiatic toad (*Bufo gargarizans*). *PeerJ*. 2022 Feb 22;10:e12993.
 3. Li W, Lan Y, Wang L, He L, Tang R, Price M, Yue B*, **Fan Z***. Comparative transcriptomes of nine tissues for the Heilongjiang brown frog (*Rana amurensis*). *Scientific Reports* 2022 December; 12: 20759.
 4. Tang R#, Wang J#, Zhou M, Lan Y, Jiang L, Price M, Yue B, Li D, **Fan Z***. Comprehensive analysis of lncRNA and mRNA expression changes in Tibetan chicken lung tissue between three developmental stages. *Animal Genetics* 2020 Oct;51(5):731-740.
 5. Bu P, Jian Z, Koshy J, Shen Y, Yue B, **Fan Z***. The olfactory subgenome and specific odor recognition in forest musk deer. *Animal Genetics* 2019 Aug;50(4):358-366.
 6. Zhou C, Zhang W, Wen Q, Bu P, Gao J, Wang G, Jin J, Song Y, Sun X, Zhang Y, Jiang X, Yu H, Peng C, Shen Y, Price M, Li J, Zhang X, **Fan Z***, Yue B*. Comparative Genomics Reveals the Genetic Mechanisms of Musk Secretion and Adaptive Immunity in Chinese Forest Musk Deer. *Genome Biology and Evolution* 2019 Apr 1;11(4):1019-1032.
 7. **Fan Z***, Li W#, Jin J, Cui K, Yan C, Peng C, Jian Z, Bu P, Price M, Zhang X, Shen Y, Li J, Qi W*, Yue B*. The draft genome sequence of forest musk deer (*Moschus berezovskii*). *GigaScience*. 2018 Apr 1;7(4):giy038. (5年平均IF = 9.3)

◆ 微生物和生物医学相关研究

1. Song J#, Dong X#, Lan Y, Lu Y, Liu X, Kang X, Huang Z, Yue B, Liu Y, Ma W, Zhang L, Yan H, He M, **Fan Z***, Guo T*. Interpretation of vaginal metagenomic characteristics in different types of vaginitis. *mSystems*. 2024 Mar 19;9(3):e0137723. (5年平均IF = 7.3)
2. Wang X#, Li J#, Li Y#, Lv M, Dong X, **Fan Z***, Guo T*. Single-cell analysis of the cellular landscape of vulvar melanoma provides new insight for immunotherapy administration. *BMC Cancer*. 2024 Jan 17;24(1):101.
3. Liu X#, He G#, Lan Y, Guo W, Liu X, Li J, Liu A, He M, Liu X, **Fan Z***, Zhang Y*. Virome and metagenomic analysis reveal the distinct distribution of microbiota in human fetal gut during gestation. *Frontiers in Immunology* 2023 Jan 5;13:1079294.
4. Li P#, Jiang J#, Li Y, Lan Y, Yang F, Wang J, Xie Y, Xiong F, Wu J, Liu H, * **Fan Z***. Metagenomic analysis reveals distinct changes in the gut microbiome of obese Chinese children. *BMC Genomics*. 2023 Nov 29;24(1):721.
5. Zhao M#, Li Y#, Gao Z, Liu A, Li Y, Li S, Gao L, Lan Y, Huang M, Wan J, He W, Mao W, Cai J, Zhou J, Yin Y, Guo Y, Zhong Q, Huang Y, Chen L, **Fan Z***, He M*. Plasma metagenomics reveals regional variations of emerging and re-emerging pathogens in Chinese blood donors with an emphasis on human parvovirus B19. *One Health*. 2023 Jul 13;17:100602.
6. Du L#, Dong X#, Song J, Lei T, Liu X, Lan Y, Liu X, Wang J, Yue B, He M, **Fan Z***, Guo T*. Temporal and spatial differences in the vaginal microbiome of Chinese healthy women. *PeerJ*. 2023 Dec 1;11:e16438.
7. Li P#, He L#, Lan Y, Fang J*, **Fan Z***, Li Y. Intrauterine Growth Restriction Induces Adulthood Chronic Metabolic Disorder in Cardiac and Skeletal Muscles. *Frontiers in Nutrition* 2022 Jul 22;9:929943.
8. Liu A, Liu X, Lu Y, Gao Z, Tang R, Huang Y, Zheng L*, **Fan Z***, He M*. Two chronically misdiagnosed patients infected with *Nocardia cyriacigeorgica* accurately diagnosed by whole genome resequencing. *Frontiers in Cellular and Infection Microbiology* 2022 Oct 12;12:1032669.

◆ 软件和数据库开发相关研究

1. Du L, Liu Q, Zhao K, Tang J, Zhang X, Yue B*, **Fan Z***. PSMD: An extensive database for pan-species microsatellite investigation and marker development. *Molecular Ecology Resources* 2020 Jan;20(1):283-291. (大类一区)

类一区TOP期刊；5年平均IF= 8.0)

2. Du L[#], Guo T[#], Liu Q, Li J, Zhang X, Xing J, Yue B, Li J*, **Fan Z***. MACSNVdb: a high-quality SNV database for interspecies genetic divergence investigation among macaques. *Database (Oxford)*. 2020 Jan 1;2020:baaa027.