

***Edwardsiella ictaluri* Almost Completely Occupies the Gut Microbiota of Fish Suffering from Enteric Septicemia of Catfish (Esc)**

Jicheng Yang ^{1,2}, Yaoyao Lin ^{2,3}, Zhaohui Wei ⁴, Zhenbing Wu ^{2,5}, Qianqian Zhang ^{2,6}, Jingwen Hao ^{2,3}, Shuyi Wang ^{2,3} and Aihua Li ^{2,3,6,*}

¹ College of Fisheries and Life Science, Dalian Ocean University, Dalian 116023, China; yangjc@ihb.ac.cn (J.Y.)

² State Key Laboratory of Freshwater Ecology and Biotechnology, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan 430072, China; linyaoyao@ihb.ac.cn (Y.L.); zqq@ihb.ac.cn (Q.Z.); haojingwen@ihb.ac.cn (J.H.); wangsy@ihb.ac.cn (S.W.); wuzhenbing@ihb.ac.cn (Z.W.)

³ University of Chinese Academy of Sciences, Beijing 100049, China

⁴ Wuhan Institute of Fishery, Wuhan 430072, China; jb-158@163.com (Z.W.)

⁵ School of Environmental Science and Engineering, Huazhong University of Science and Technology, Wuhan 430074, China

⁶ National Aquatic Biological Resource Center, NABRC, Wuhan 430072, China

* Correspondence: liaihua@ihb.ac.cn; Tel.: 86-27-68780053

Table S1. Number of sequences analyzed, observed diversity richness (OTUs), estimated OTU richness (Chao1), diversity index (Shannon and Simpson), and estimated sample coverage for 16S rRNA libraries of the different samples. H1~H3 stand for the intestinal samples of the healthy fish, and D1~D6 stand for the intestinal samples of the diseased fish, and W1, W2 for the water sample of Diseased and healthy ponds, respectively.

Sample	OTU	Shannon	Simpson	Chao1	Coverage (%)
H1	215	2.15	0.24	223	99.96
H2	276	1.09	0.69	293	99.90
H3	171	1.37	0.51	196	99.88
D1	46	0.03	0.99	58	99.94
D2	65	0.09	0.98	88	99.92
D3	53	0.17	0.95	65	99.94
D4	43	0.04	0.99	84	99.91
D5	41	0.03	0.99	52	99.94
D6	49	0.04	0.99	72	99.93
W1	477	4.16	0.03	550	99.69
W2	466	4.22	0.03	529	99.75

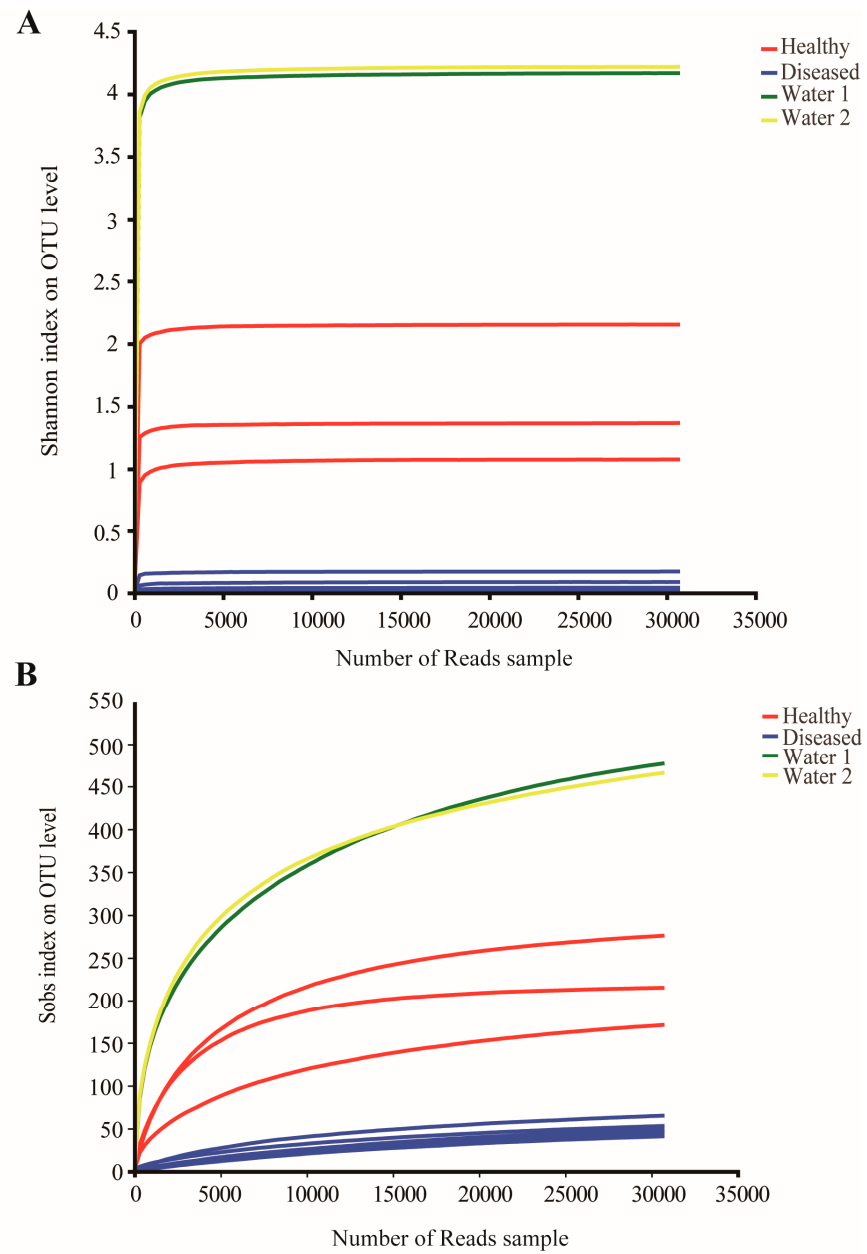


Figure S1. Rarefaction analyses of OTUs clustered at 97% sequence identity of all samples: **(A)** Shannon curves on OTU level of the intestinal and water sample; **(B)** Rarefaction curves on OTU level of the intestinal and water sample.

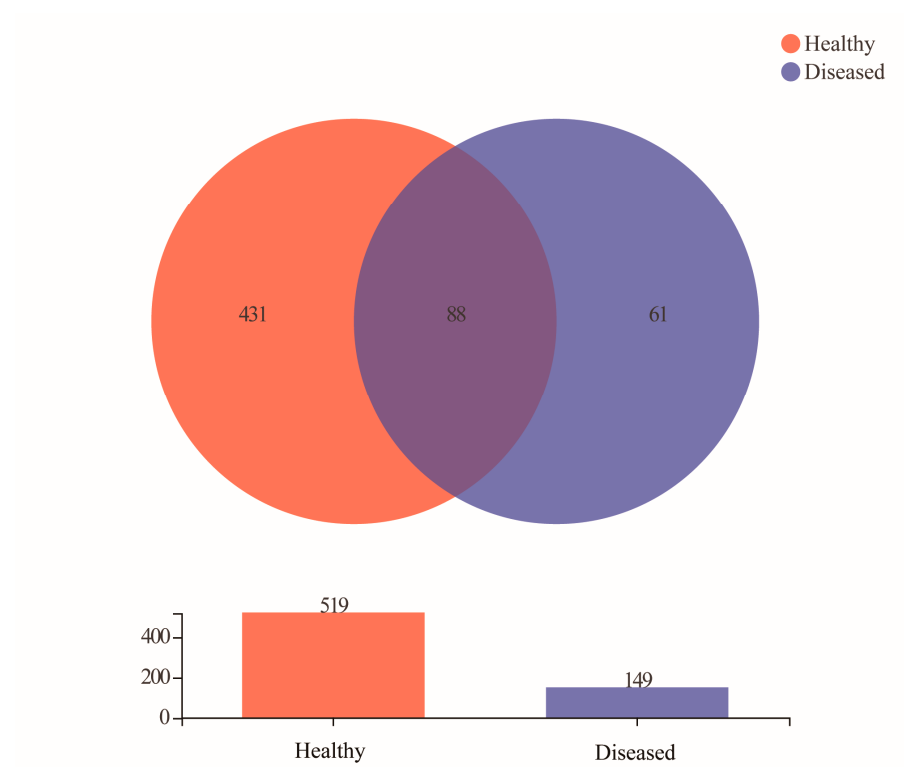


Figure S2. The Venn diagram showing the numbers of OTUs that were shared and unique in the gut communities (97% sequence identity); Healthy and Diseased represent the intestinal samples of healthy and diseased fish.