

## **SUPPLEMENTAL INFORMATION: CONTENTS SUMMARY**

### ***SUPPLEMENTAL FIGURES:***

*Figure S1:* We use 16S rRNA gene T-RFLP analysis to reveal interindividual and interlocation variation in the zebrafish intestinal microbiota.

*Figure S2:* We use 16S rRNA gene sequence-based phylogenetic analysis to show that *Edwardsiella* spp. are common members of the intestinal microbiota of recently-caught zebrafish and wild yellow catfish.

### ***SUPPLEMENTAL TABLES:***

*Table S1:* We provide a detailed description of the clone library and pyrosequencing datasets generated and used in this study.

*Table S2:* We provide estimates of alpha-diversity in the 16S rRNA gene sequence datasets used in this study.

*Table S3:* We provide a comprehensive classification of the 16S rRNA gene sequence datasets using the RDP-II Naïve Bayesian Classifier tool.

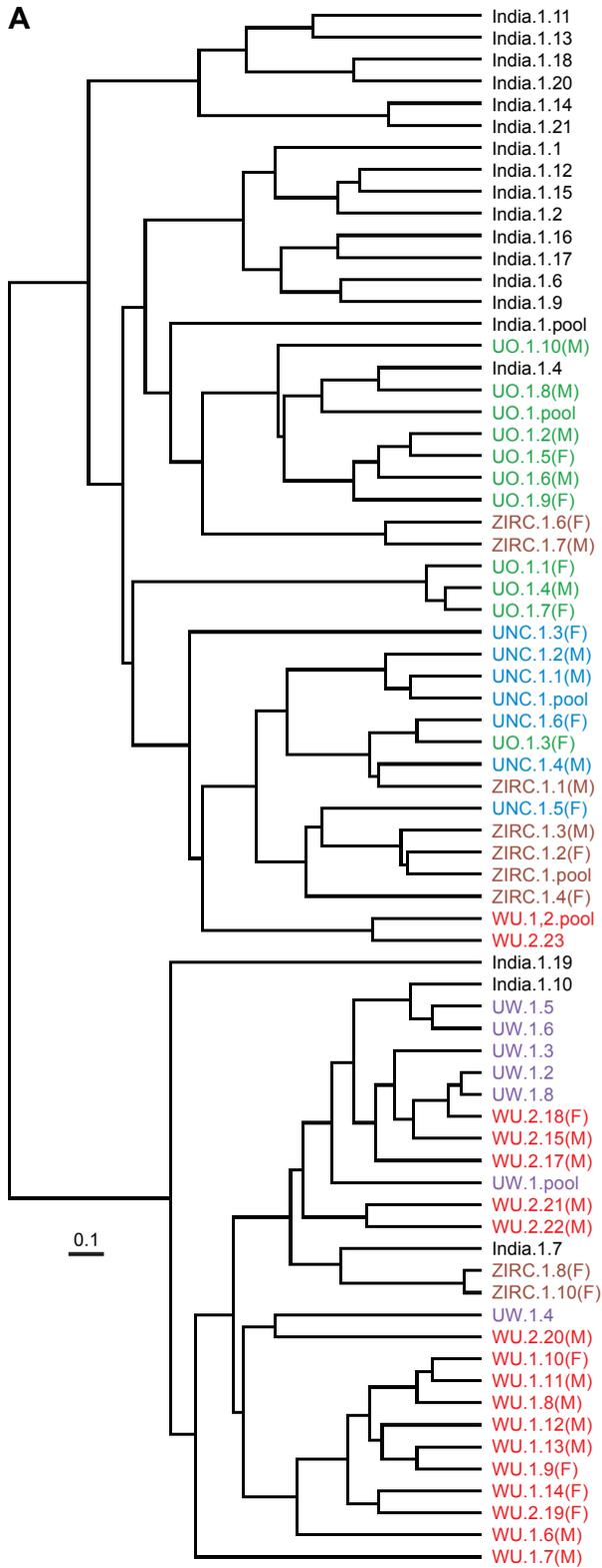
*Table S4:* We provide a list of the bacterial genera shared among intestinal microbiotas of recently-caught and domesticated zebrafish as revealed by pyrosequencing of 16S rRNA gene amplicon pools.

*Table S5:* We list the modified PCR primers used for pyrosequencing in this study.

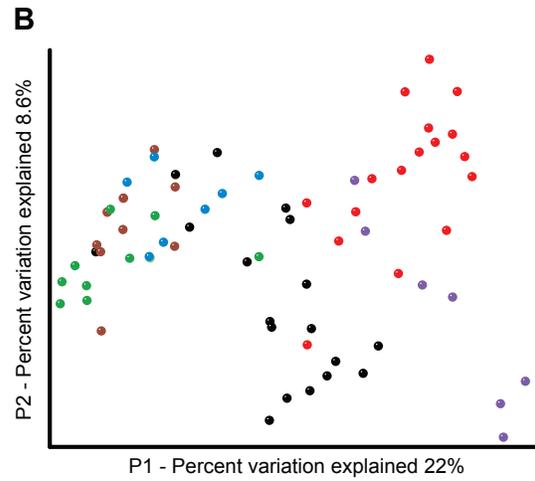
## SUPPLEMENTAL FIGURES:

### **Figure S1: 16S rRNA gene T-RFLP analysis reveals interindividual and interlocation variation in**

**the zebrafish intestinal microbiota.** (A) Relatedness of intestinal microbiotas from adult zebrafish collected from different locations revealed by a hierarchical cluster analysis of T-RFLP profiles (see Table 1). Intestinal samples from individual zebrafish (e.g., India.1.1) or pooled individual zebrafish (e.g., India.1.pool) are color coded according to their location. Male (M) and female (F) fish are labeled where known. The branch length from each node is defined as the Pearson distance between the samples being compared. The scale bar on the tree measures a distance of 0.1, where a difference of 1 would mean that two profiles are completely uncorrelated. (B) Individual T-RFLP samples clustered on an unweighted PCoA plot based on a Pearson distance matrix. (C) Matrix of average T-RFLP Pearson distances within and between fish from different locations.



India = West Bengal, India  
 UO = University of Oregon, Eugene, OR  
 ZIRC = Zebrafish International Resource Center, Eugene, OR  
 UW = University of Washington, Seattle, WA  
 WU = Washinton University, St. Louis, MO  
 UNC = University of North Carolina, Chapel Hill, NC



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	India	UO	ZIRC	UW	WU	UNC
India	0.39	0.43	0.51	0.60	0.66	0.51
UO	0.43	0.29	0.39	0.84	0.77	0.37
ZIRC	0.51	0.39	0.34	0.87	0.79	0.33
UW	0.60	0.84	0.87	0.32	0.55	0.79
WU	0.66	0.77	0.79	0.55	0.46	0.67
UNC	0.46	0.37	0.33	0.79	0.67	0.24

Average Pearson Distance:



**Figure S2: 16S rRNA gene sequence-based phylogenetic analysis reveals that *Edwardsiella* spp. are common members of the intestinal microbiota in recently-caught zebrafish and wild yellow catfish.** Maximum likelihood tree showing the phylogenetic affiliation of *Edwardsiella* 16S rRNA gene sequences from uncultured and cultured bacteria derived from the intestinal contents of recently-caught zebrafish (*Danio rerio*, red text) and wild yellow catfish (*Pelteobagrus fulvidraco*, blue text), and those from other sources available in the public databases (black text). Bootstrap support ( $\geq 50\%$ ) is shown as results from 1000 bootstrap replicates. The scale bar indicates 0.05% estimated sequence divergence.

