

Fluctuation of gut microbiome in *Cirrhinus mrigala* is associated with changes in dissolve oxygen of water

Authors: Chandana Basak¹, Nibendu Mondal², Sumit Chatterjee², Wriddhiman Ghosh², Ranadhir Chakraborty^{1*}

Affiliations: ¹ OMICS Laboratory, Department of Biotechnology, University of North Bengal, Siliguri-734013, West Bengal, India.

²Department of Microbiology, Bose Institute, P-1/12 CIT Scheme VII M, Kolkata 700054, India.

*Corresponding author. E-mail: rcnbusiliguri@gmail.com

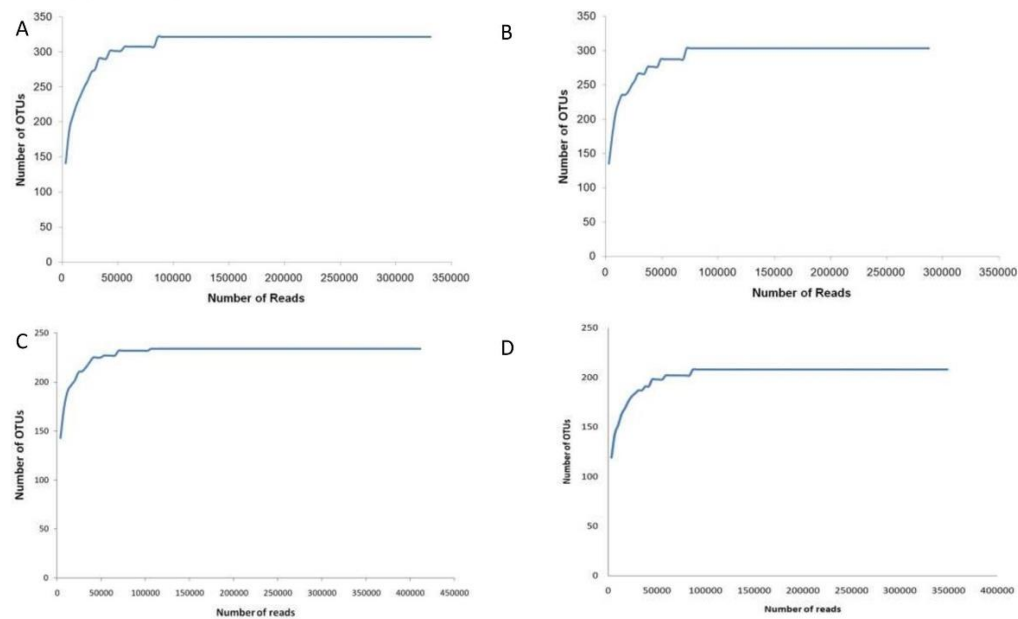
Supplementary data:

Fig. S1 Rarefaction curves showing the proportionality between OTU-level diversity and the number of V3 regions in 16S rRNA gene sequence reads analyzed for (A) MCA, (B)MCP, (C) MTA or (D) MTP samples. For each sample, number of reads used in OTU-clustering is plotted along the X-axis, while number of OTUs is plotted along the Y-axis

Fig. S2 Dendrogram analysis of control and experimental samples of *C. mrigala* at phylum level in MicrobiomeAnalyst using the Bray-Curtis distance method. MCA: Anterior gut of *C. mrigala* under control condition, MCP: Posterior gut of *C. mrigala* under control condition, MTA: Anterior gut of *C. mrigala* under test condition, MTP: Posterior gut of *C. mrigala* under test condition

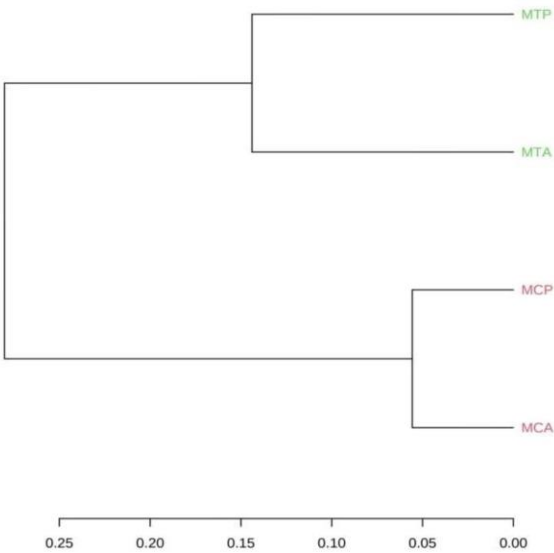
Fig. S3 Stacked bar depicting abundance of diverse bacteria at order level in anterior and posterior gut samples of *C. mrigala* under control and experimental conditions. Here X axis showing the name of bacterial order while number of OTUs is plotted along the Y-axis

Figure S1_ Supplementary data



57
58
59
60
61
62
63
64
65
66
67
68
69
70

Figure S2_ Supplementary data



71
72
73
74
75
76

Figure S3_ Supplementary data

