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Data Article

16S rRNA amplicon sequencing dataset for conventionalized and conventionally raised zebrafish larvae

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ABSTRACT

Data presented here contains metagenomic analysis regarding the sequential conventionalization of germ-free zebrafish embryos. Zebrafish embryos that underwent a germ-free sterilization process immediately after fertilization were promptly exposed to and raised to larval stage in conventional fish water. At 6 days post-fertilization (dpf), these "conventionalized" larvae were compared to zebrafish larvae that were raised in conventional fish water never undergoing the initial sterilization process. Bacterial 16S rRNA amplicon sequencing was performed on DNA isolated from homogenates of the larvae revealing distinct microbiota variations between the two groups. The dataset described here is also related to the research article entitled "Microbial modulation of behavior and stress responses in zebrafish larvae" (Davis et al., 2016) [1].

Specifications Table

Subject area	*Biology* *Microbiome analysis in zebrafish larvae*

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More specific subject area	
Type of data	*Table*
How data was acquired	*Illumina MiSeq*
Data format	*Raw, analyzed*
Experimental factors	*Reconstitution of sterilized embryos with conventional microbial populations*
Experimental features	1) *Microbial DNA extraction and amplification via PCR* 2) *Bacterial 16S rRNA amplicon sequencing* 3) *Trimming, filtering, and annotation of sequence data*
Data source location	*Columbia, MO, USA* *Latitude: 38.901366 Longitude: −92.2825 Altitude: 246* m
Data accessibility	Data is within this article and available via http://www.ncbi.nlm.nih.gov/bioproject/321905

Value of the data

- The data presented here can be used as justification for the use of zebrafish larvae as a model species in gnotobiotic research.
- These data are valuable in illustrating the consistency of microbial taxa present within a given group of larvae.
- These data will be of use in the selection of an appropriate methodology to generate gnotobiotic zebrafish larvae.

1. Data

Data presented here represent results of 16S rRNA sequencing of V4 region amplicons, generated using the Illumina MiSeq platform. Data are presented at the taxonomic levels of phylum, family, and operational taxonomic unit, and represent an average coverage of 4235 reads per sample (Table 1). This paper contains data related to the research concurrently published in Davis et al. [1].

2. Experimental design, materials and methods

2.1. Production of conventionalized and conventionally-raised zebrafish larvae

Wild-type zebrafish breeders were placed into a breeding tank overnight to spawn. Embryos were collected immediately after fertilization and evenly divided into separate groups for subsequent treatment. Conventionalized (CV) embryos were generated by following a previously published method [2]. Briefly, embryos were collected in sterile fish water containing 250 mg/mL amphotericin B, 5 μg/mL kanamycin, and 100 μg/mL ampicillin (AB-fish water). After sorting to remove unfertilized embryos, viable embryos were transferred to a tissue culture hood and gently washed 3 times in AB-fish water. Embryos were immersed in 0.1% PVP-Iodine solution for 2 min, and then immediately washed 3 times with sterile fish water. After washing, the embryos were immersed in 0.003% bleach solution for 1 h before being washed an additional 3 times with sterile fish water. Finally, the embryos were transferred into sterile tissue culture flasks containing conventional fish water. Conventionally raised (CR) embryos were transferred and maintained in conventional fish water immediately after collection without undergoing the sterilization process. All zebrafish embryos were maintained in a