

**Dataset title:** Diazotroph abundances in the water column

**Chief Scientist on cruise:** Cécile Guieu & Sophie Bonnet

**Data Originator(s):** Mar Benavides, Sophie Bonnet, Ilana Berman-Frank

**Institute(s):** M.I.O. Aix-Marseille Université, Univ. Toulon, CNRS,  
IRD UMR235 (UM110) Marseille, France

**Contact email(s):** mar.benavides@ird.fr

**Additional contributors:**

**Project:** TONGA

**Funded by:** ANR, LEFE, Fond FOF, AMIDEX, IRD

**Dataset abstract:** Diazotroph groups were quantified in the Western Tropical South Pacific accross trophic and trace metal gradients to investigate the role of trace metals from shallow underwater volcanoes on such activities. This includes samples collected on depth profiles taken at 12 stations, including 2 volcanoes and 2 mooring stations

**Sampling protocol/ collection details:** Seawater was sampled from go flo bottles attached to a Trace Metal Clean Rosette at 12 stations and 6 depths/station in 2.25 L (1/2 gallon) acid-washed polycarbonate bottles. The samples were filtered on 0.2 µm polysulfone filters and stored in bead beater cryotubes vials at -80°C until analysis onshore.

**Analytical protocol/ method:** DNA is extracted from the filters using a mini-plant kit (Qiagen) as specified in Moisander et al. (2008). DNA extracts are used to quantify nifH gene copies of 5 groups of diazotrophs (UCYN-A1, UCYN-B, UCYN-C, Trichodesmium and Gamma) using TaqMan qPCR assays and previously published primer-probe sets. The reactions are run in 25 µL consist of 12.5 µL TaqMan PCR Master Mix (Applied Biosystems), 0.5 µL of the forward and reverse primers (at 10 µM, HPLC purified, Eurofins), 0.25 µL probe (at 10 µM, Eurofins), 9.25 µL PCR grade water, 0.25 µL bovine serum albumin (BSA, at 10.08 µg µL<sup>-1</sup>), and 1 µL standard or sample. The qPCR reaction is run on a CFX96 Touch Real-Time PCR Detection System (BioRad). Amplification efficiencies are tested for all reactions. Standard curves are calculated by linear regression of threshold cycle (Ct) and log gene copies per reaction using duplicate standards ranging from 10<sup>7</sup> or 10<sup>8</sup> to 10<sup>0</sup> gene copies. Duplicate no template control wells are included in all runs. Inhibition tests are carried out for all samples by adding 1 µL of the 10<sup>5</sup> standard to each sample well. The limits of detection and quantification are considered as 1 and 8 gene copies per reaction, respectively.