Original data for the paper:

ACUTE AND CHRONIC RESPONSE TO A CHANGE IN SALINITY OF THE EURYHALINE POLYCHAETE *PYGOSPIO ELEGANS (CLAPARÈDE)*

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SUMMARY:
These data were collected in an experimental study designed to evaluate the ability of the polychaete *Pygospio elegans* to cope with an acute as well as a long-term change in salinity. Specimens from Herslev, Denmark, originating from a salinity of about 15 were exposed to salinity 15 as control and 5 and 30 as low and high salinity treatments. After acute exposure, we measured body volume changes as well as gene expression of seven genes related to volume- and osmoregulation within 4 hours of exposure.

METHODS:
Body volume
Mean body volume [µm^3] standard deviation (SD) and standard error (SE) of specimens of *Pygospio elegans* were measured before and during 7 days after exposure to salinity 5, 15 and 30. One individual at a time was placed in a 1.6 ml well of 11 mm diameter containing seawater of the respective salinity under a dissecting microscope fitted with a video camera. The first 4 hours of exposure were documented using a time lapse video, afterwards single pictures were taken daily. In some cases, when automated measurements were impossible, only five pictures for each time point were measured manually. For the measurement an approximate cylinder shape was assumed so that body volume was calculated as V = L * (W/2) 2 * π. Several pictures per time point were taken and the volume averaged. Measurements were performed using the software BR v. 4.2 (Nikon, RAMCON A/S Birkerød, DK).
ddPCR data
Expression of 9 genes of interest in 10 specimens of *Pygospio elegans* were measured after exposure to salinity 5, 15 or 30 for either 45 min or 240 min/4 hours (6 treatments: 5-45, 5-240, 15-45, 15-240, 30-45, 30-240) was measured using the QX200TM digital droplet PCR system. Number of positive and negative droplets, absolute concentration with lower and upper confidence interval and mean copies per partition of the 1/10 diluted cDNA template were determined after correction of the baseline of fluorescence intensity via the R script ddpcRquant.

DATA DESCRIPTION:

Two data sheets are present in the data file: one describing “Body volume data” and the other describing “ddPCR data”.

Body volume

Each treatment, Salinity 5, 15 (control) and 30, are indicated in the Table header. For each of the 10 worms per treatment measured, we report an individual identification numer (ID), mean volume, standard deviation, standard error, number of images measured and comments made during measurement at each time point. Mean volume was calculated before exposure and then from one picture per second for 30 seconds immediately and then after 5, 10, 20, 30, 45, 60, 90, 120, 150, 180, 210, 240 minutes of exposure to the tested salinities.

ddPCR data

The name of each studied gene is shown in the Table header. For each, there is a code for sample name which represents tested salinity – exposure time – worm ID, e.g. Worm 4 exposed to salinity 15 for 240 minutes translates into 15-240-4. The ddPCR data include: number of positive droplets, number of total droplets, concentration [copies/µl], as well as its lowerC I and upper CI, and the mean number of copies of the target gene per partition (λ). This estimate, $\lambda = -\ln(1 - k/n)$; k = number of positive droplets and n = total number of droplets (according to Hugget et al. 2013 MIQE guidelines), was used in analysis of gene expression reported in the study. Values in italics indicate that subsequent analysis (normalization and statistical analyses) were performed on the average of several measurements of the same sample.