S1 Supplementary materials and methods

S1.1 Procedure for counting cells using a Morphologi G3

The Morphologi G3 is an automated tool for characterization of particles in a variety of dry and wet mixtures including soils and/or solutions based on their shape and size (0.5 µm to several mm) (Fig. S1). This instrument was successfully used for the purpose of counting the cells by discriminating trichomes from other particles in the seawater matrix based on defined properties (e.g. elongation, circularity and fibers width). The Morphologi G3 instrument basically comprises three major parts: (a) wet cell (Fig. S2); (b) scanning area including the microscope optics (2.5X, 5X, 10X, 20X and 50X) and wet-cell sample holder (Fig. S3); and (c) software. The performance of the instrument is based on establishment of a standard operating procedure (SOP), including the software adjustments which need to be performed to ensure that all trichomes have been identified by the instrument. The entire procedure for cell counting using the Morphologi G3 can be summarized by the following steps:

(i) Measurement control – fixed number of slides/plates and a new result for each slide/plate,

(ii) Sample carrier – wet cell plate (100×80×0.125 mm) and compensate for plate tilt,

(iii) Illumination settings –discopic (bottom light), 80 calibration intensity and 0.5 intensity tolerance,

(iv) Optics selection (2.5X),

(v) Threshold (adjusted based on the best contrast between trichomes and background),

(vi) Scanned area (mm^2) – is determined based on the culture density (e.g. bigger scanned area for less dense cultures),

(vii) Analysis settings –analysis ID 3, minimum pixels 50, calculate fiber parameters,

(viii) Filters –to exclude/classify the scanned particles based on the defined properties at specific range (e.g. area (pixels) less than 100, fiber elongation less than 0.8, fiber width less than 8 and circularity greater than 0.5),

(ix) Gentle injection (to prevent introduction of tiny bubbles) of about 2.5 mm of well-mixed cell suspension (fixed with 1percent Lugol's iodine) into the wet cell (Fig. S4), placement into cell holder and start of particle counting (Fig. S5), and

(x) Afterwards, the instrument provides a library of images of each individual particle (in this case trichomes) by scanning the sample underneath the microscope optics, while keeping the particles in focus. It is also able to measure a range of morphological properties (e.g. fiber length) for each particle (Fig. S6).

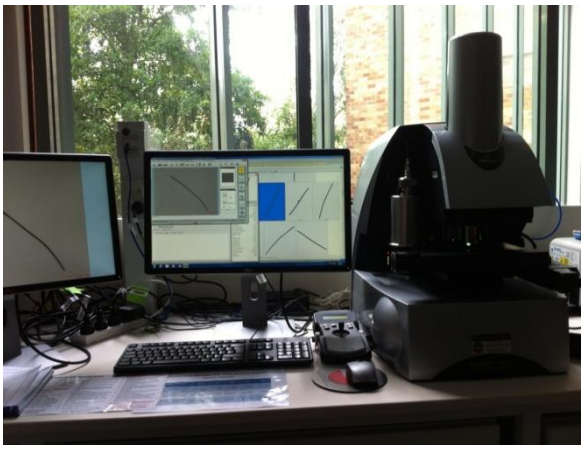

Figure S1. Morphologi G3 instrument

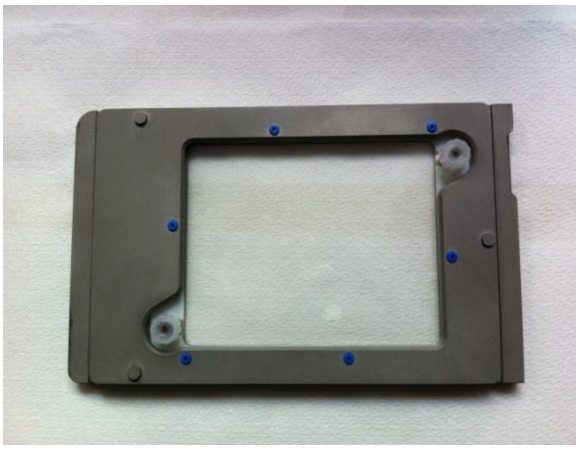

Figure S2. Wet cell

Figure S3. Scanning area

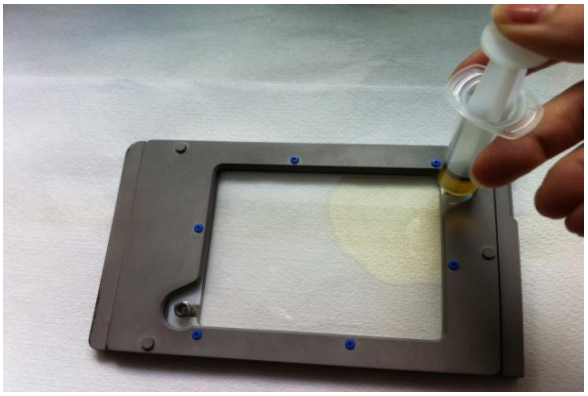

Figure S4. Injection of sample

Figure S5. Placing wet cell

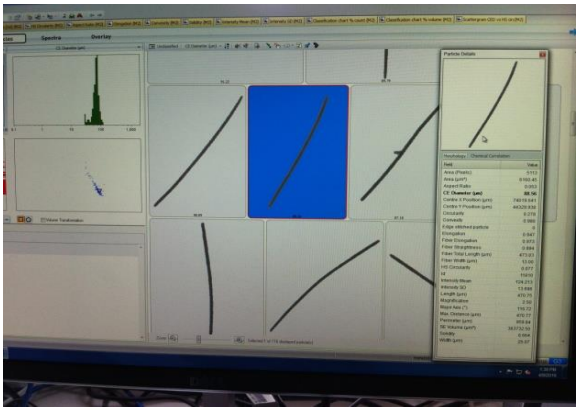

Figure S6. Library of images

S1.2 Procedure for calculation of growth rates using Morphology G3 data

To calculate number of cells per mL, initially the measured lengths for all the trichomes were summed to obtain the total length (µm) and then this value was divided by the average length of a cell (µm) to get total number of cells. The average length of cell was calculated by dividing total length of several trichomes (at least three) by their number of cells (counted annually using the 20X objective lens). The number of cells was then divided by volume in mL (i.e. scanned area (mm2) ×0.25 mm (gap between the cell glasses)/1000) to obtain number of cell mL^{-1}. The growth rate (µ) was then calculated from equation below,

$$\mu = \frac{(ln(f) - ln(i))}{d} \qquad \text{(S1)}$$

where d, f and i represent, respectively, number of days, final and initial cell densities, respectively.

S1.3 Data analysis and calibration

For a better understanding of the data analysis procedure, an example is illustrated for data obtained by addition of 20 nmol L^{-1} of Fe(II) into a sample. As shown in Fig. S7, a time period of 70 s is required to load and mix sample with the reagent prior to obtaining a stable reading. This duration, which is shown in red, is excluded from further data analysis while the remaining data (i.e. 70-600 s) are extrapolated back to time zero via linear regression on a plot of log signal versus time (Fig. S8).

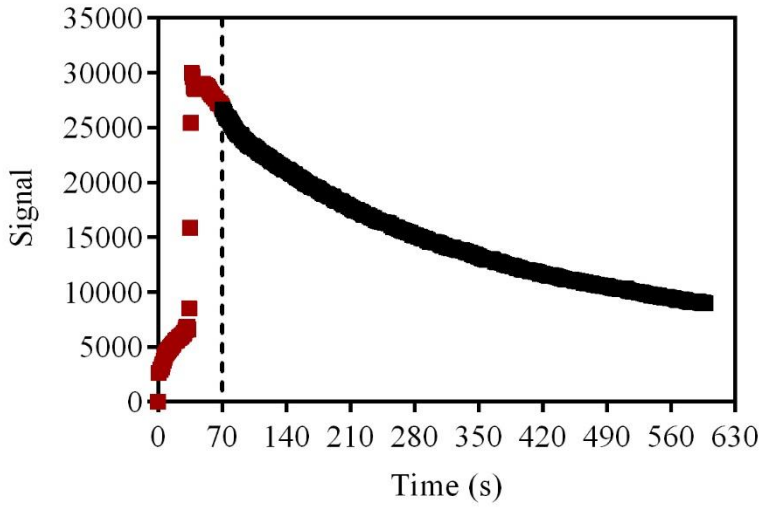

Figure S7. Display of primary data points collected by the chemiluminescence system. Red and black colours illustrate, respectively, data values excluded from and included in subsequent data analysis. The curve represents the mean from two replicates.

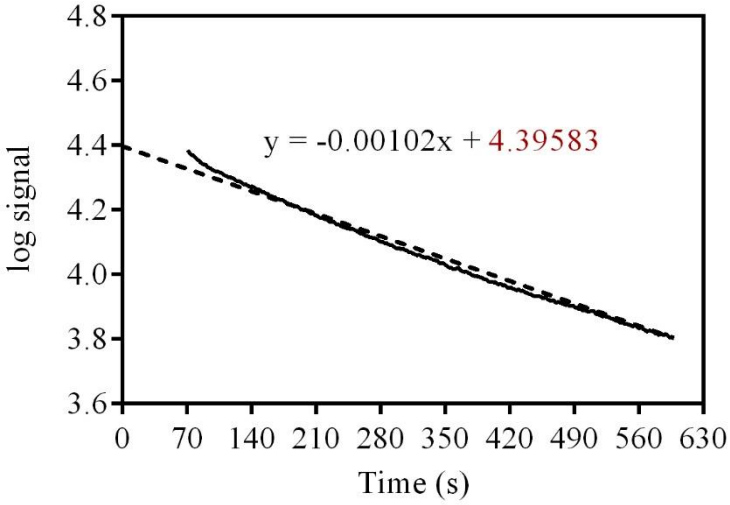

Figure S8. Plot of log signal versus time illustrating extrapolation procedure. The dashed line shows the extrapolated data points at intervals of 70-600 s to time zero. The equation of the line contains the slope and the Fe(II) concentration at time zero/intercept (highlighted in red).

S2 Supplementary results

Table S1. Comparison between Fe(II) oxidation rate constants in the presence and in the absence of organic exudates obtained using linear regression and kinetic modelling.

Type of ligand	Culture age (d)	Ligand concentration (µmol L^{-1})	$k' \times 10^4$ (s^{-1}) (from linear regression)	k (mol^{-1} s^{-1}) (from kinetic modelling)
ASW (no ligand)	N/A	N/A	6.2	5.9
EDTA	N/A	0.5	5.1	12
EDTA	N/A	20	7.8	12
Organic exudates from culture containing 1.44-2.03 nmol L^{-1} Fe´	2	Unknown	9.8	10
	4		9.1	7.6
	6		9.7	12
	8		8.0	8.6
	10		8.9	9.0
	12		9.7	9.2
	15		8.9	8.5
	17		9.1	7.6
	19		6.4	5.5
	25		7.9	7.6
Organic exudates from culture containing 0.05-0.29 nmol L^{-1} Fe´	2	Unknown	11	12
	4		10	10
	6		11	12
	8		12	7.8
	10		12	10
	12		9.4	8.4
	15		4.7	6.9
	17		9.3	7.9
	19		9.4	6.2
	25		7.0	12