Electronic Supplementary Material (ESI) for RSC Advances.

Supporting Information

Biosynthesis Enhancement of Tropodithietic Acid (TDA) Antibacterial Compound through Biofilm Formation by Marine Bacteria Phaeobacter inhibens on Micro-Structured Polymer Surfaces

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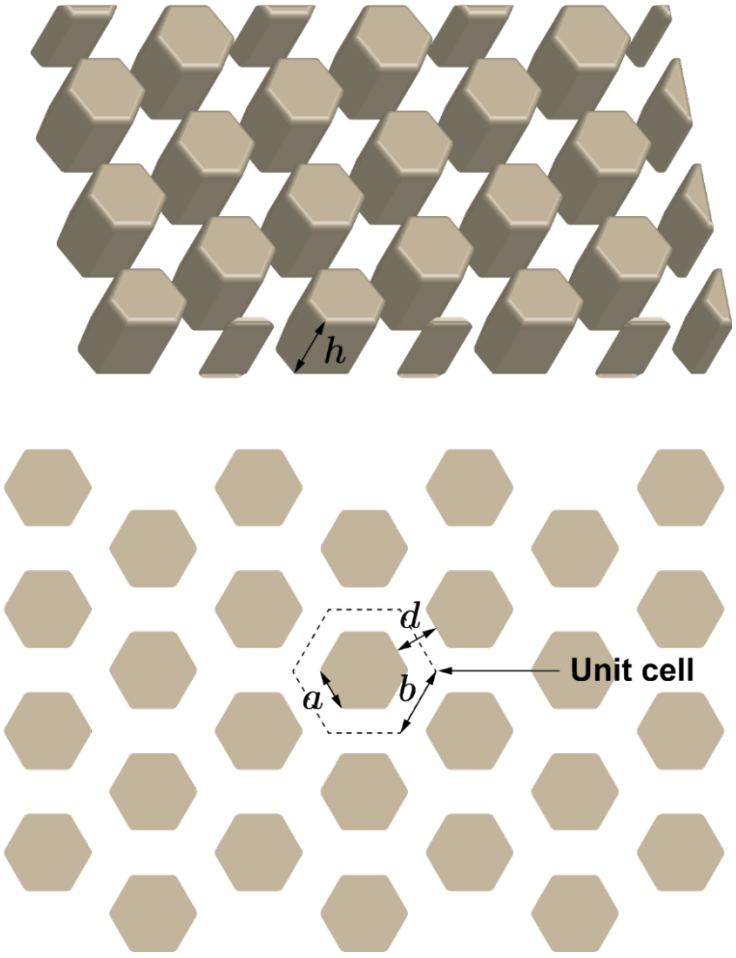

Figure S1. Calculation of surface area factors. Both the pit and pillar structures can be built from hexagon shaped unit cells with side lengths $\boldsymbol{b}$. For both surfaces, the hexagon side length $\boldsymbol{a}$ was 5 µm, however, the widths of sidewalls between neighbour pits, $\boldsymbol{d}$ was 5 µm, whereas for pillars the trenches between neighbour pillars, $\boldsymbol{d}$ was 10 µm. For both microstructure geometries, the depth/height was $\boldsymbol{h} \approx 12$ µm. The area of the shown unit cell can thus be computed from $\boldsymbol{S_{uc}} = \frac{3\sqrt{3}}{2}\boldsymbol{b^2}$, with $\boldsymbol{b} = \boldsymbol{a} + \frac{\boldsymbol{d}}{\sqrt{3}}$. The real surface area inside each unit cell, however, also comprises the areas of six sidewall of the hexagonal pits and pillars. With $\boldsymbol{S_{sw}} = \boldsymbol{ah}$, the surface factor expressing the fraction of the real surface area to the projected surface area can then be computed as $\boldsymbol{r} = \frac{\boldsymbol{S_{uc}+6S_{sw}}}{\boldsymbol{S_{uc}}}$.

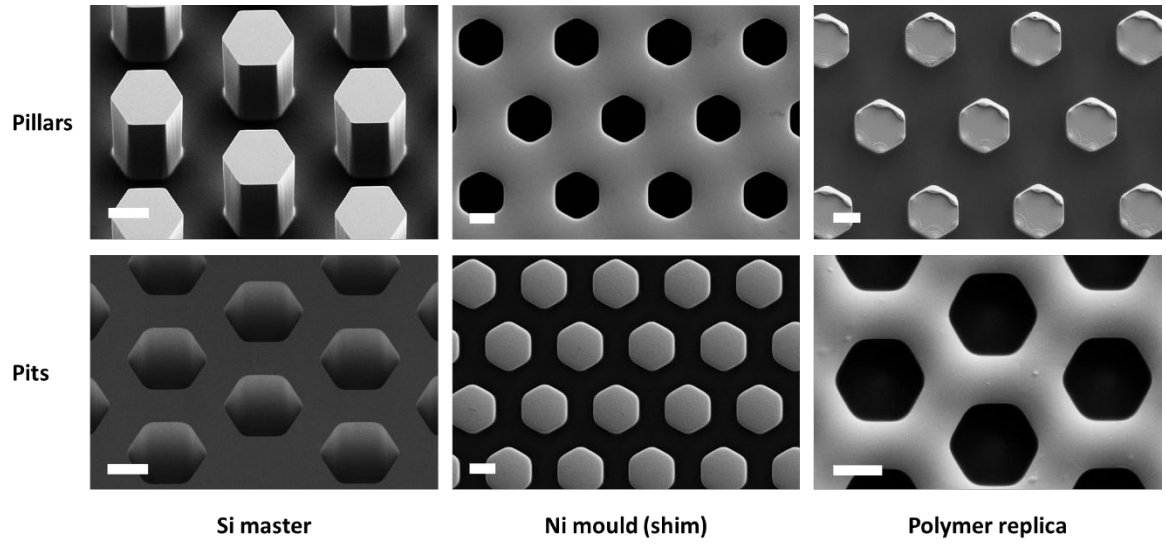

Figure S2. SEM micrographs showing the three fabrication steps of the pillar and pit surfaces Scale bars in all images represent 5 µm. In the first step, the structures were originated on a silicon surfaces, by steps of photo-lithography and dry etching. In the second step, a Ni mould with a reversed relief polarity was electroformed on the Si master. The final polymeric replicas were finally fabricated by injection moulding, using the Ni electroformed structured shims as a mould.

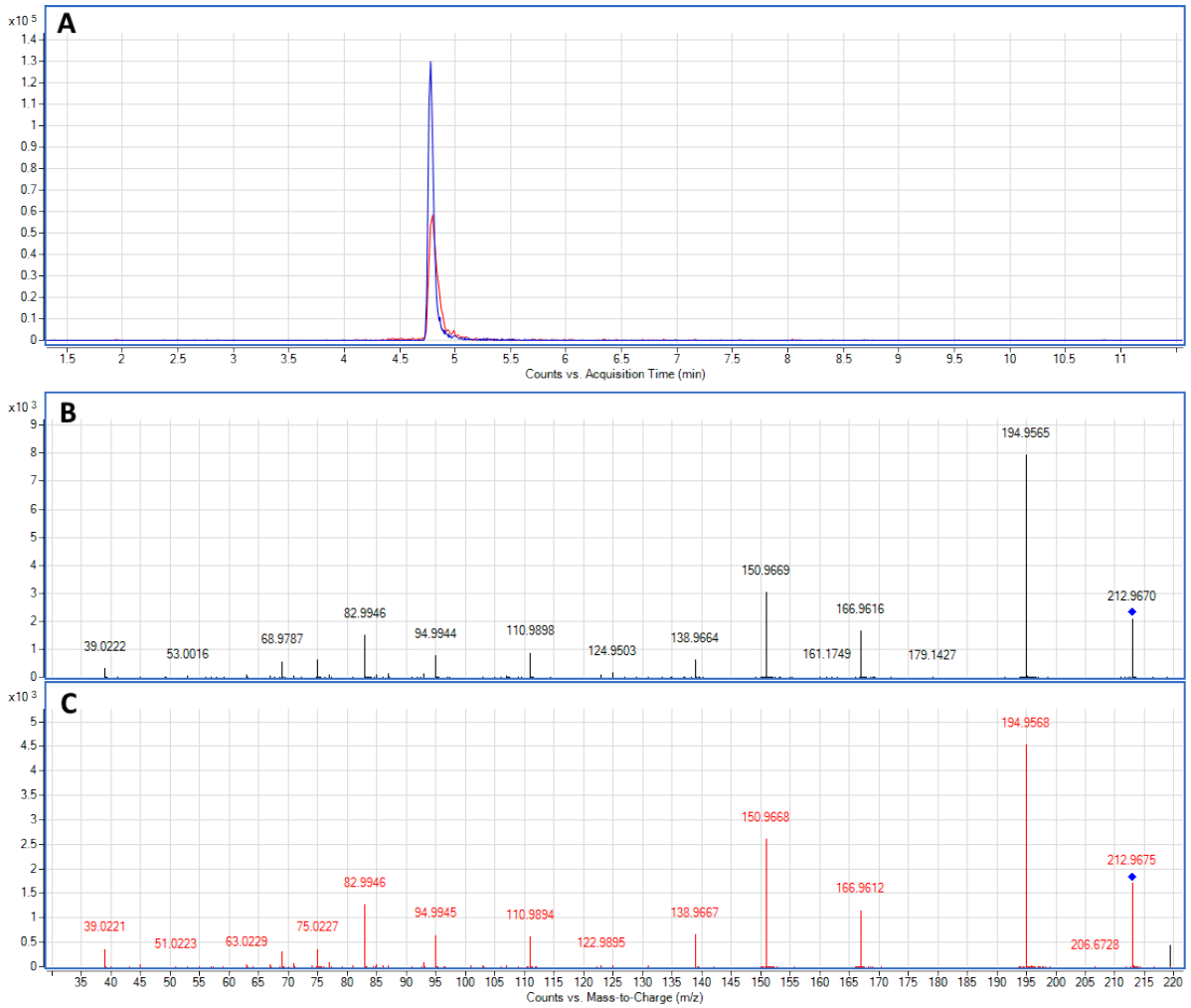

Figure S3. **A:** Overlay of extracted ion chromatograms at m/z 212.9675±0.005 within the TDA reference standard sample (red) and a representative culture extract (blue).
B: Fragmentation pattern of the m/z 212.9675 ion within the TDA reference standard.
C: Fragmentation pattern of the m/z 212.9675 ion within a representative culture extract.

Table S1. Correlation coefficients were calculated with the following formula for the Pearson correlation coefficent, where x-values are the levels of biomass, and y-values are the TDA counts:

$$r = \frac{\sum(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum(x_i - \bar{x})^2 \sum(y_i - \bar{y})^2}}$$

Day/Surface	Planar	Pits	Pillars
2	-0.61761	-0.31609	-0.5073
4	0.462754	-0.09034	0.526148
6	0.11652	-0.2452	0.041022
7	-0.23054	-0.27988	-0.48349
8	0.190542	-0.39097	-0.25576

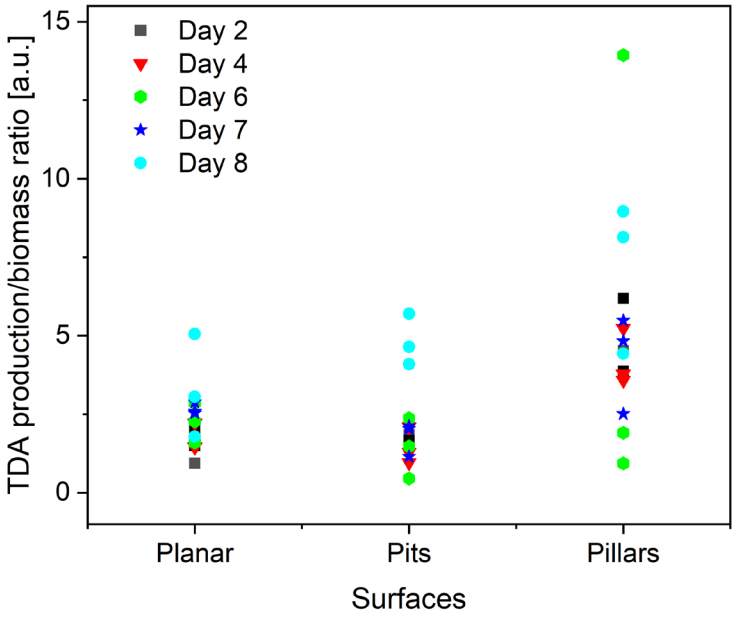

Figure S4. The ratios of TDA production to Biomass were calculated. From different surfaces, in each day, at least 7 datapoints were collected from each of 3 flow cells and averaged. The ratio was calculated with TDA production for each of the surfaces in the three flow cells divided by the corresponding biomass averages. The three datapoints with same colour for each surface shown in the figure correspond to data obtained from the three flow cells. Regardless of the culture days, the ratio from the pillar surface always shows a higher value, which indicates that the pillar surface support higher TDA production with less biomass when compared to the other surfaces.