

Journal of Visualized Experiments

Use of a High-throughput In Vitro Microfluidic System to Develop Oral Multi-Species Biofilms --Manuscript Draft--

Manuscript Number:	JoVE52467R1
Full Title:	Use of a High-throughput In Vitro Microfluidic System to Develop Oral Multi-Species Biofilms
Article Type:	Invited Methods Article - JoVE Produced Video
Keywords:	dental plaque, biofilm, confocal laser scanning microscopy, three-dimensional structure, pyrosequencing, image analysis, microfluidic, saliva, COMSTAT, IMARIS, IMAGEJ,
Manuscript Classifications:	10.1.897.520: Miniaturization; 10.1.897.724: Technology, Dental; 2.3: Bacteria; 5.5.595.395: Microscopy, Confocal; 7.6.120: Biofilms
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Abstract:	<p>There are few high-throughput in vitro systems which facilitate the development of multi-species biofilms that contain numerous species commonly detected within in vivo oral biofilms. Furthermore, a system that uses natural human saliva as the nutrient source, instead of artificial media, is particularly desirable in order to support the expression of cellular and biofilm-specific properties that mimic the in vivo communities. We describe a method for the development of multi-species oral biofilms that are comparable, with respect to species composition, to supragingival dental plaque, under conditions similar to the human oral cavity. Specifically, this methods article will describe how a commercially available microfluidic system can be adapted to facilitate the growth of multi-species oral biofilms derived from a pooled saliva inoculum and grown in pooled cell free human saliva. Furthermore, a description of how the system can be used in conjunction with a confocal laser scanning microscope to generate 3-D biofilm reconstructions for architectural and viability analyses will be presented. Given the broad diversity of microorganisms that grow in the environmentally germane microfluidic-based oral biofilms (including Streptococcus, Neisseria, Veillonella, Gemella, and Porphyromonas), a protocol will also be presented describing how to harvest microfluidic-developed biofilm cells for further subculture- or DNA extraction and analysis. The limits of both the microfluidic biofilm system and the current state-of-the-art data analyses will be addressed. Ultimately, it is envisioned that this article will provide a baseline technique that will improve the study of oral biofilms and aid in the development of additional technologies that can be integrated with the microfluidic platform.</p>
Author Comments:	Concerning timelines, I would like to have filming completed by the end of August 2014

	because of teaching commitments. Also, we have grants due for review in late September/early October and potentially another in December and would like the paper in Press by September and published before the end of the year, if found to be acceptable.
Additional Information:	
Question	Response
If this article needs to be "in-press" by a certain date to satisfy grant requirements, please indicate the date below and explain in your cover letter.	Sep 22, 2014
If this article needs to be filmed by a certain date to due to author/equipment/lab availability, please indicate the date below and explain in your cover letter.	Aug 29, 2014

Title:

Use of a High-throughput In Vitro Microfluidic System to Develop Oral Multi-Species Biofilms

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RUNNING TITLE:

An oral multi-species microfluidic biofilm system

KEY WORDS:

Dental plaque, biofilm, confocal laser scanning microscopy, three-dimensional structure, pyrosequencing, image analysis, image reconstruction, saliva, modeling, COMSTAT, IMARIS, IMAGEJ, multi-species biofilm communities.

SHORT ABSTRACT:

The goal of this methods paper is to describe the use of a microfluidic system for the development of multi-species biofilms that contain species typically identified in human supragingival dental plaque. Methods to describe biofilm architecture, biofilm viability, and approach to harvest biofilm for culture- or culture-independent analyses are highlighted.

LONG ABSTRACT:

There are few high-throughput *in vitro* systems which facilitate the development of multi-species biofilms that contain numerous species commonly detected within *in vivo* oral biofilms. Furthermore, a system that uses natural human saliva as the nutrient source, instead of artificial media, is particularly desirable in order to support the expression of cellular and biofilm-specific properties that mimic the *in vivo* communities. We describe a method for the development of multi-species oral biofilms that are comparable, with respect to species composition, to supragingival dental plaque, under conditions similar to the human oral cavity. Specifically, this methods article will describe how a commercially available microfluidic system can be adapted to facilitate the growth of multi-species oral biofilms derived from a pooled saliva inoculum and grown in pooled cell free human saliva. Furthermore, a description of how the system can be used in conjunction with a confocal laser scanning microscope to generate 3-D biofilm reconstructions for architectural and viability analyses will be presented. Given the broad diversity of microorganisms that grow in the environmentally germane microfluidic-based oral biofilms (including *Streptococcus*, *Neisseria*, *Veillonella*, *Gemella*, and *Porphyromonas*), a protocol will also be presented describing how to harvest microfluidic-developed biofilm cells for further subculture- or DNA extraction and analysis. The limits of both the microfluidic biofilm system and the current state-of-the-art data analyses will be addressed. Ultimately, it is envisioned that this article will provide a baseline technique that will improve the study of oral biofilms and aid in the development of additional technologies that can be integrated with the microfluidic platform.

INTRODUCTION:

Biofilms are architecturally complex communities of bacteria that are aggregated on surfaces¹. These communities typically contain numerous species that interact with one another, within the biofilm, and with the environment². Oral biofilms, the most visually conspicuous being dental plaque, are a persistent problem in humans and their uncontrolled development leads to taxonomically diverse multi-species communities³. The component bacteria of these diverse communities can be up to 1000-times more resistant to antimicrobials than their free-floating (planktonic) counterparts⁴⁻⁶. Failure to treat these oral biofilm communities, which can cause dental caries and periodontal disease, has resulted in a significant public health burden: over 500 million visits to the dentist office per annum in the US, and an approximately \$108 billion to treat or prevent periodontal disease and dental caries⁷.

92 “While many microbiologists advocate studying microbial behavior under natural
93 conditions, few of them do so. This is because their morale for overcoming the
94 difficulties is constantly sapped by the attractive ease of working with laboratory
95 cultures.” Smith⁸.
96

97 At present, oral biofilm research is conducted using a variety of *in vivo* and *in vitro*
98 approaches, each with their own advantages and disadvantages^{9,10}. *In vitro*
99 approaches often use model biofilm systems that are relatively easy to set up but may
100 lack clinical/real-world relevance^{10,11}. *In vivo* approaches typically rely upon animal
101 model systems that may reproduce certain aspects of the human oral environment, but
102 again suffer from limitations due to differences in anatomy, physiology, microbiology
103 and immunology between animals and humans^{12,13}. It should be noted that oral biofilms
104 can also be developed on enamel surfaces held in a stent within the mouths of human
105 volunteers, but this approach is currently relatively costly and labor-intensive^{14,15}.
106 Ultimately, novel agents or technologies to improve oral healthcare are tested in
107 humans under controlled clinical trial conditions¹¹. At present, an often-used *modus*
108 *operandi* for identifying and evaluating new oral healthcare agents is to perform
109 laboratory studies first, to discern potential efficacy, and then perform animal studies
110 and “field trials” that employ clinicians to evaluate the success of the technology^{9,16,17}.
111 Unfortunately, lab studies tend to rely on model systems that occupy a large footprint,
112 are technologically challenging to use, and often contain simplified communities of one
113 or at most a few species to derive potential real-world meaning^{10,18}. Given that dental
114 plaque biofilms, and indeed nearly all biofilms in the broader environment, contain
115 multiple species and develop in a complex milieu under flow, developing biofilms that
116 contain one or a few species in artificial media is likely to provide outcomes that are not
117 representative of the real-world scenario^{10,19}. To address the time, cost, training
118 requirements, and the poor representative nature of laboratory model biofilm systems to
119 the real-world environment, we recently developed a high throughput and
120 environmentally germane biofilm system²⁰ (Fig. 1). The system benefits from the use of
121 cell-free pooled human saliva (CFS) as medium and untreated pooled human (bacterial)
122 cell-containing saliva (CCS) as an inoculum. Uniquely, the system also combines
123 microfluidic technology, a confocal laser scanning microscopy platform, and culture-
124 independent bacterial diversity analysis technology. Taken together, the model system
125 is environmentally germane (using saliva as an inoculum to grow multi-species biofilms
126 at 37°C in flowing saliva) and the oral biofilms contain species (including *Streptococcus*,
127 *Neisseria*, *Veillonella*, and *Porphyromonas* species) in abundances representative of
128 those found in early supragingival plaque²⁰.
129

130 When considering this work that describes the use of the newly developed model
131 system, particular attention to the amalgamation of CLSM, microfluidics, and the
132 capability to perform culture-independent diversity analyses must be given. The union of
133 these technologies by our research group was intentional and not only adds a high-
134 throughput capability to the newly developed model system but also allows questions to
135 be asked that could not be easily addressed before with other systems. Firstly, CLSM
136 has distinct advantages over traditional microscopy as it allows for the three-
137 dimensional analysis of biofilms. Often unappreciated, this is extremely important as

138 biofilms are heterogeneous with respect to species composition and spatial position as
139 well as the physiological conditions being imposed at different spatial locations within
140 the biofilm^{6,21}. In concert with three-dimensional rendering software and image analysis
141 software, the biofilm architecture, spatial relationships between composition species,
142 and extent of antimicrobial killing can be analyzed²²⁻²⁴. Such abilities are not possible
143 using standard transmitted light or epifluorescence microscopy. Next, microfluidics has
144 garnered particular attention in the field of microbiology as it enables the study of
145 biofilms under carefully controlled conditions (flow, temperature, pH, etc) and only
146 requires small volumes of liquid²⁵⁻²⁷. As a point of comparison, growing an oral biofilm
147 in human saliva within a flow cell model system (a system that is arguably considered
148 the mainstay model for many oral biofilm studies) for 22 hours at a similar flow-rate and
149 shear as that achieved in a microfluidic system requires at least 200 mL, as opposed to
150 800 µL in the microfluidic device²⁸⁻³¹. Thus, a microfluidic model biofilm system enables
151 the study of quantity-limited material under defined conditions. Finally, pyrosequencing
152 technology has been optimized in the last decade to require only small amounts of
153 material to perform a community analysis and is sufficiently versatile to control depth of
154 sequencing to obtain the identity of even rare biofilm species. The use of this
155 technology, such as bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP),
156 has allowed for pertinent questions concerning the ecology of biofilms to be addressed
157^{32,33}. Such questions imbued difficulties in the past when pyrosequencing was not
158 available because of the time and costs required to create plasmid libraries and the
159 complex technological and analytical steps required to derive data^{33,34}. Of course, a
160 great advantage with culture-independent approaches, such as pyrosequencing, is that
161 the bacterial species that cannot be grown in isolation conventional laboratory media
162 (i.e. viable but non-cultivable species) can be identified and their relative abundance in
163 the community quantified^{35 36}. To add perspective, as early as 1963, the late Sigmund
164 Socransky estimated that approximately 50% of the bacteria in material isolated from
165 the human oral gingival crevicular crevice could not be cultured using laboratory growth
166 conditions³⁷.

167
168 The objective of this methods paper is to describe the approach to develop oral multi-
169 species biofilms in a commercially available microfluidic (Bioflux) system under
170 conditions representative of the human oral cavity and with a species composition and
171 abundance that is comparable to supragingival plaque. Furthermore, using both
172 freeware and commercial software, we highlight how basic biofilm architecture
173 measures can be derived from CLSM data, with a focus on approaches to quantify
174 biofilm biomass, roughness, and viability (based upon Live/Dead staining). Finally, the
175 steps required to harvest biofilm material for diversity analysis by bTEFAP are
176 described.

177 178 **PROTOCOLS:**

179 With regard to institutional reviews for human subject work of this type, prior
180 arrangements and permissions should be garnered from the host institution. As an aid
181 to preparing an application, a useful NIH algorithm/chart can be found
182 here:[http://grants1.nih.gov/grants/policy/hs/PrivateInfoOrBioSpecimensDecisionChart.p](http://grants1.nih.gov/grants/policy/hs/PrivateInfoOrBioSpecimensDecisionChart.pdf)
183 [df](http://grants1.nih.gov/grants/policy/hs/PrivateInfoOrBioSpecimensDecisionChart.pdf)

1) PREPARATION OF POOLED SALIVA FOR USE AS AN ENVIRONMENTALLY GERMANE GROWTH MEDIUM

1.1. Recruit ≥ 5 individuals for saliva donation. Do not take any identifying information, ensure no individuals will donate saliva if they are ill, or have taken oral antibiotics in the past 3 months, or have consumed food or liquid, with the exception of water, in the previous 2 hours before donation.

1.2. Collect saliva in 50 mL plastic tubes. Pool the collected saliva in a plastic beaker, keeping it on ice. Do not use glass as polymers in the saliva will adhere to the internal glass surfaces

1.3. Add Dithiothreitol (DTT) to a final concentration of 2.5 mM from a 100X stock. (Stock is frozen in single-use aliquots at -20°C). Stir for 10 minutes in a plastic beaker on ice.

1.4. In order to remove particulate matter, centrifuge the pooled saliva in a Sorval SS-34 centrifuge for 30 minutes at $17,500 \times g$.

1.5. Dilute the saliva with 3 volumes of dH_2O to give one-fourth concentrated saliva.

1.6. Filter-sterilize saliva using $0.22 \mu\text{m}$ polyethersulfone (PES), low protein binding filter. Use filter with large surface area, or use several small area filters. Keep saliva in a plastic container on ice while filtering.

1.7. Freeze the pooled saliva at -80°C in 50 mL plastic tubes until needed to grow bacteria. Each plastic tube is for one use only and should contain no more than 35 mL as each microfluidic well holds a maximum of 1.2 mL ($1.2 \text{ mL} \times 24 \text{ wells} = 28.8 \text{ mL}$) and space is needed in each tube as frozen saliva expands during freezing.

1.8. For use, thaw the pooled saliva at room temperature. Once thawed, filter-sterilize once more ($0.22 \mu\text{m}$ polyethersulfone, low protein binding filter to remove any precipitates).

2) PREPARATION OF POOLED SALIVA FOR USE AS AN INOCULUM

2.1. Recruit ≥ 5 individuals for saliva donation. Do not take any identifying information, ensure no individuals will donate saliva if they are ill, have taken oral antibiotics in the past 3 months, or have consumed food or liquid, with the exception of water, in the previous 2 hours before donation. Samples should be collected over 30 min.

2.2. Collect saliva in 50 mL plastic tubes at room temperature and pool the collected saliva in a plastic beaker at room temperature.

229 2.3. Dilute pooled saliva with autoclaved general reagent grade glycerol to yield a stock
230 with a final ratio of 25% glycerol, 75% cell-containing saliva [CCS].

231
232 2.4. Freeze saliva at -80°C in 3 mL single-use aliquots until needed.

233
234 2.5. When required to inoculate the microfluidic system, aliquots are thawed at room
235 temperature and agitated gently on a vortexer for 5 seconds before being pipetted into
236 the microfluidic system as described in step 3 of the protocol, below.

237 **3) GROWTH OF ORAL MULTI-SPECIES BIOFILMS**

238
239 3.1. *CFS pre-treatment* – First coat the channels with CFS. Add 100 μL of CFS to each
240 outlet well, do this by using an automatic experimental controls software, such as
241 Bioflux by selecting “manual” and set flow from channels “B1-B24” to be used.

242
243 3.2. Next, set shear to 1.0 dyne/cm² and flow for 2 minutes at room temperature to
244 ensure homogenous distribution of the CFS throughout the channel. Ensure there is
245 fluid in each inlet channel to verify that CFS flowed through all channels evenly.

246
247 3.3. Incubate plate at room temperature for 20 minutes.

248
249 3.4. Aspirate out CFS/pretreat solution that remains in the outlet wells and transfer to
250 the inlet wells. This total ~ 100 μL will serve to balance against the pressure being
251 applied to the inoculum in the outlet well.

252
253 3.5. *Inoculation* – To each outlet well, add 100 μL of CCS inoculum. Place the
254 microfluidic plate on the heat plate set at 37°C , select manual within the control software
255 and set flow from outlet wells to the inlet wells (ie reverse) at 1.0 dyne/cm² for exactly 6
256 seconds.

257
258 3.6. Incubate plate on heating plate at 37°C for 40 min to allow for initial adherence and
259 growth of the inoculum.

260
261 3.7. *Overnight Growth* - Aspirate all of the inoculum from each of the outlet wells for
262 channels being used. Add up to 1 mL total volume of CFS into each of the inlet wells
263 (can be done on top of existing CFS).

264
265 3.8. Incubate the plate on the heating plate at 37°C , select manual and set the program
266 to run at 0.2 dyne/cm² for 22 hours.

267
268 3.9. *Stain prewash* - Aspirate all fluid from the inlet and outlet wells and add 100 μL of
269 PBS (pH 7.4) to each of the inlet wells. Flow for 20 minutes at 0.2 dyne/cm².

270
271 3.10. *Stain mixture addition* – For cell viability staining make 100 μL of stain mixture for
272 each channel to be stained. Specifically, Add 3 μL of SYTO 9 and 3 μL of propidium
273 iodide per 1mL of PBS using commercial cell viability staining kit such as LIVE/DEAD.
274

This generates a staining mixture containing 10.02 μM of SYTO 9 and 60 μM of propidium iodide.

3.11. Aspirate the remaining PBS from the inlet wells and then add 100 μL of the cell viability stain mixture to each inlet well. Set to flow at 0.2 dyne/cm^2 and run the solution from inlet to outlet for 45 minutes at room temperature.

3.12. . *Post-staining wash* - Aspirate the remaining stain in each of the inlet wells and add 100 μL of PBS to each inlet well. Set to flow at 0.2 dyne/cm^2 and run the PBS solution from inlet to outlet for 30 minutes at room temperature to remove any excess stain.

4) IMAGE COLLECTION, 3D RENDERING, AND IMAGE ANALYSIS

4.1 Use an inverted confocal laser scanning microscope (CLSM) to highlight key steps and considerations when collecting biofilm data from the microfluidic system.

NOTE: Given the dimensions of the microfluidic channels, the need for sensitivity to discern biofilm structure, and the requirements to detect fluorescence signal of varying intensity, the fit the CLSM with a 40X 1.25NA objective lens or one with similar optical quality, magnification, and numerical aperture.

4.2. Standardize the emission capture gates with gain and offset measurements being kept constant. Ensure that the laser power does not exceed 25% as this will result in photo-bleaching.

4.3 Convert CLSM files from the Leica Image File type (LIF) to OME (Open Microscopy Environment) file type. This allows for greater ease of access and compatibility between software programs. Use commercially available software such as, IMARIS to convert files to this type.

3D Rendering for Images/Figures

4.4. Once converted to OME format, use IMARIS to render the images in 3D. Perform this using a combination of “*Easy3D*” and “*Surpass*” options.

NOTE: Attention to background signal and thresholding should be made. The histogram function in IMARIS can be used to obtain the collection range and this should be kept constant between images being analyzed.

4.5. Save images as different file types using the “*snapshot*” function and make careful consideration to image resolution before saving file types.

4.6 Assemble images into figures using software such as CorelDraw or Adobe Illustrator.

3D Image Analysis for Graphs and Tables

4.7 Use freely available IMAGEJ²³ and COMSTAT/COMSTAT 2³⁸ for this 3D image analysis. Download the packages from <http://rsb.info.nih.gov/ij/> and <http://comstat.dk/>, respectively.

NOTE: The software platform JAVA will need to be installed prior to the use of the image analysis software.

4.7.1. Use the IMAGEJ software with COMSTAT2 plugin and the most recent Java update installed. Import the OME files for each biofilm image in “*hyperstack*” mode and view with “*split channels*”.

4.7.2. Analyze individually the two channels (red/propidium-iodide/dead being channel 0, green/SYTO-9/LIVE being channel 1) using the “*histogram*” function of IMAGEJ. This function lists the total number of pixels of 8-bit OME files (shown as “count”) at each color intensity from 0-255 (shown as “value”), with 0 being pixels with no signal (background) and 255 being pixels with complete signal saturation.

4.7.3. Export the data into Microsoft Excel and standardize all signal values by weighting each pixel by the corresponding signal intensity. This is performed by multiplying the total count at a given signal intensity by the numerical 8-bit value (0-255) of that signal intensity.

4.7.4. Sum all weighted values, 0-255, for both channels for each biofilm image captured. Take the sum of the weighted values for both channels and find the percent total signal from either channel, do this to determine the relative ratio or percent red and percent green signal (i.e. the percent “DEAD” and percent “LIVE” for each treatment).

4.7.5. Perform statistical analyses, for example using two-tailed Student's T-test modified for unequal variance. Values of $p < 0.05$ are considered significant and those values of $p < 0.01$ are considered highly significant.

5) HARVESTING BIOFILM CELLS FOR CULTURE-INDEPENDENT ANALYSIS

5.1 Remove all spent and unused saliva from inlet and outlet wells. Wash the wells with 1 mL sterile distilled water three times.

5.3. Add 100 μ L of sterile distilled water to the inlet wells and, using the software control interface, pass the sterile distilled water forward through the channels at ≥ 8.0 dyne/cm² (flow rate ≥ 745 μ L/h, shear of 800 s⁻¹) for at least 10 min. Repeat in the reverse direction for at least 10 minutes and then repeat the forward and reverse washing step process.

5.4. Check by light or by epifluorescence microscopy (if cells were stained/labelled) for thorough biofilm removal (Fig. 2). Collect the 100 μ L cell-suspension and store at -80°C for culture-independent analysis. A cost-effective analysis of community composition can be through using bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP) using the approach described in Nance et al.²⁰

FIGURE AND TABLE LEGENDS:

Figure. 1. The Bioflux microfluidic CSLM oral biofilm system. (A) A diagram showing a vertical cross-section of the Bioflux system while being mounted on a Leica SPE CLSM. (B) An annotated (black lines) photograph highlighting two microfluidic channels and the inlet and outlet wells. (C) An example of a rendered two-dimensional Live/Dead stained oral biofilm that has been treated with a 0.01% CPC solution resulting in heterogeneous killing, in part due to reaction diffusion limitation. Green color indicates live cells, stained with Syto 9; red colored cells are dead or damaged and stained with propidium iodide. Fig 1A and 1B from Nance et al.²⁰ with permission. Bar in Fig. 1C represents 30 μ m.

Figure. 2. Two dimensional and three-dimensional views of rendered 22 h biofilms developed in pooled cell-free saliva (CFS) that was inoculated from pooled cell-containing saliva (CCS). An untreated biofilm community (left column of images) is compared against a 70% ethanol treated biofilm community and a representative biofilm is shown in different planes of view (XY, XZ, and ZYZ). Histograms showing the differences in red (dead/damaged cells) and green (live cells) are shown for each image stack (logged data shown in black and non-logged data shown in grey). All data is derived from 8 bit images and thus on a scale of 0-255 (256 increments). Scale bars represent 30 μ m.

Figure. 3. Flow chart demonstrating the outcome of extraction/harvesting of 22 h oral multi-species biofilm (developed from a CCS inoculum in flowing CFS) from the Bioflux microfluidic device using the elevated shear/flow technique. Dotted lines have been applied to the images to aid in determining the location of the channel walls. The community composition of the harvested biofilm can be analyzed by 454 pyrosequencing approaches such as bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP) and expressed at multiple taxonomic levels (phylum through species) depending upon requirements. Shown is an example of the community composition, at the phylum level, of biofilms harvested from three microfluidic channels. Bars represent scale in micrometers.

Table 1. Quantification of biofilm properties of untreated and 70% ethanol treated 22 h biofilms developed in pooled cell-free saliva (CFS) from an inoculum cell-containing saliva (CCS). Bold values are the averages and non-bolded values in brackets are the standard deviations). Data is from at-least five images from three microfluidic channels. Significant differences to the untreated control are highlighted by an asterisk (*: $P < 0.05\%$; **: $P < 0.01\%$).

REPRESENTATIVE RESULTS:

3D RENDERING OF BIOFILMS

Representative results are shown in Figure 3. A useful capability to IMARIS software is the contained tools to examine each slice of the collected biofilm stack and to render them to create three-dimensional reconstructions. In addition, artificial shadowing effects can be added to help visually interpret three-dimensional structures. Furthermore, the biofilms can be orientated in any direction with almost limitless useful magnification to explore biofilm or micro-colony structure. The images presented in Fig. 3 show the outcome of the treatment of an oral multi-species biofilm. Of particular note is that treatment with 70% ethanol resulted in significant color change for most of the biofilm (from green to red) suggesting significant cell-death or cell-damage. The large micro-colonies appeared to contain more dead cells than the underlying (and now exposed) micro-colony cells. Such an outcome is conceivably due to de-adhesion of biofilm cells because ethanol is a membrane-active antimicrobial. By converting the files to OME format and analyzing the rendered stacks in IMAGEJ, it can be seen by applying histogram functions that the amount of red and green signal is inversely proportional between the untreated biofilms and those treated with ethanol.

QUANTIFICATION OF BIOFILM PROPERTIES

Table 1 shows the average and standard deviations of key structural parameters. A key advantage to using IMARIS, IMAGEJ and COMSTAT, is that if IMARIS is used first, OME files can be generated to allow files to be pipelined through IMAGEJ and COMSTAT. The sample data presented in Table 1 shows that treatment of the oral biofilms with 70% ethanol resulted in a highly significant drop in viability from 80.8% to 28.3%. Ethanol can cause some cell damage and structural changes in biofilms but this is often-times not measurably significantly different. Here, no differences in measures of average biovolume, average thickness and average roughness were detected (Table 1).

DISCUSSION:

This methods paper highlights the basic steps required to setup and run a microfluidic system in a manner to allow for the development of oral multi-species biofilms derived from pooled saliva and grown in filter-sterilized 25% human saliva. Approaches to characterize the biofilm are given but it should be remembered that these described approaches are modifiable and additional technologies such as, for example, stains or labels can be introduced. As a matter of example, one could conceivably use labeled antibodies or introduce a fluorescent strain to visualize and examine the spatial position of certain species within the oral multi-species biofilm. Furthermore, depending upon the model of the microfluidic system being used, it is possible to develop biofilms under anaerobic conditions (in the case of the Bioflux system, a technical note is available at Fluxion.com on this subject).

A key aspect to the microfluidic systems are their compatibility with multiple technologies and this is highlighted here by the ability to perform culture-independent diversity analyses (Fig. 3). While the internal surfaces of the microfluidic system are not easily accessible, vigorous forward and reverse flow does enable substantial biofilm biomass to be removed. While all of the biofilm cannot be easily removed and this could be considered a weakness to the system, it is relevant to note that many model biofilm systems also have a similar issue and the claims from any such collected data have to

be tempered with this knowledge. For example, it is possible that the abundance of streptococci might be higher in the biofilm than actually determined because many *Streptococcus* species have exceptionally good abilities to bind to saliva coated surfaces³⁹.

As with all model biofilm systems, one has to be mindful of the questions being asked. For example, this system would not be suitable for long-term longitudinal studies. A model system such as a constant depth film reactor, a sorbarod system, or a drip reactor might be more suitable⁴⁰⁻⁴², although the problem of limited quantities of saliva for a model system becomes an issue as these are not microfluidic-based designs. In a similar light though, the Bioflux system described here could also be adapted for studies of biofilms in other environments where biological fluids are only available in small quantities. For example, this could include urine and wound exudate.

In conclusion, as with any *in vitro* model system, one has to be cognizant of the strengths and weaknesses to the model microfluidic system for the growth of oral biofilms. While the microfluidic system is arguably environmentally germane and allows for the development of biofilms that are compositionally *similar* to the *in vivo* situation, it is not the *same* as the *in vivo* situation and will likely never be so. A laboratory model system is only as good as its assumptions and while the microfluidic system has many overlaps with conditions within the human oral cavity, factors such as host-based effects and external biotic and abiotic challenges (e.g. through drinking and eating) cannot be easily replicated. With this in mind, however, it is clear that the high throughput nature, and environmental, and microbiological overlaps with the real-world oral environment make this an alluring system for making predictions before preparing for lengthy, expensive, and logistically challenging clinical studies.

ACKNOWLEDGEMENTS:

The authors thank William Nance (University of Michigan) for help developing the biofilm growth protocols and John Batista (Fluxion, San Francisco, CA) for advice concerning technological issues relating to the Bioflux system. This work was supported by the National Institutes of Health (NIH: R21DE018820 to A. H. R.) and University of Michigan start-up funds to A. H. R.

TRANSPARENCY DECLARATION:

A. H. R. and N.S.J. have received research awards from a variety of sources such as the National Institutes of Health (NIDCR), Colgate-Palmolive (Piscataway, NJ) and the Society for Applied Microbiology to fund research studies in their lab over the past five years. All other authors: none to declare.

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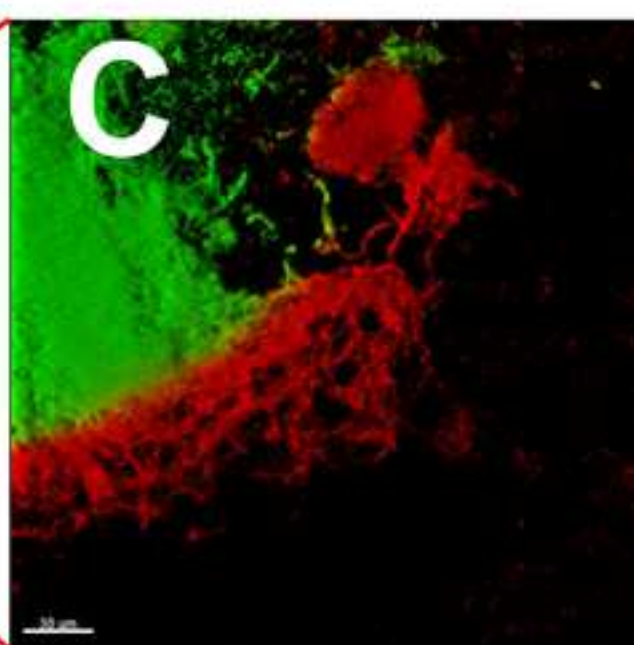
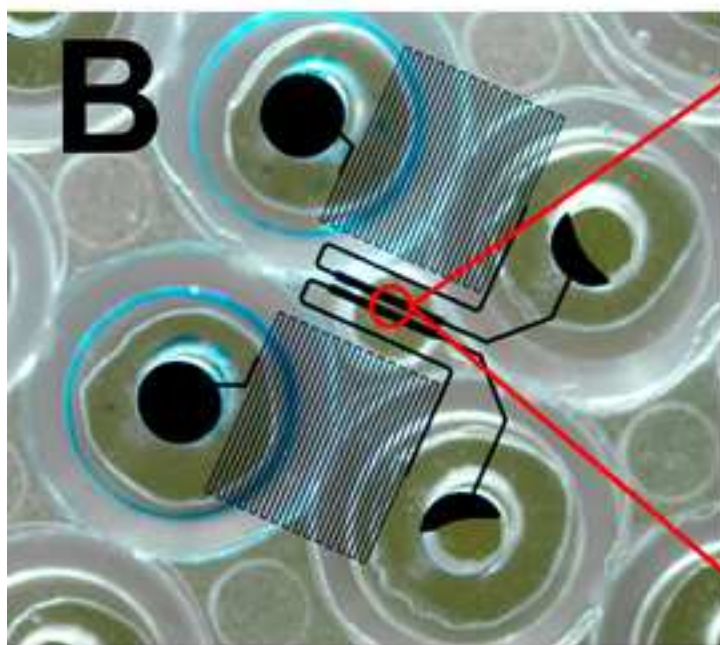
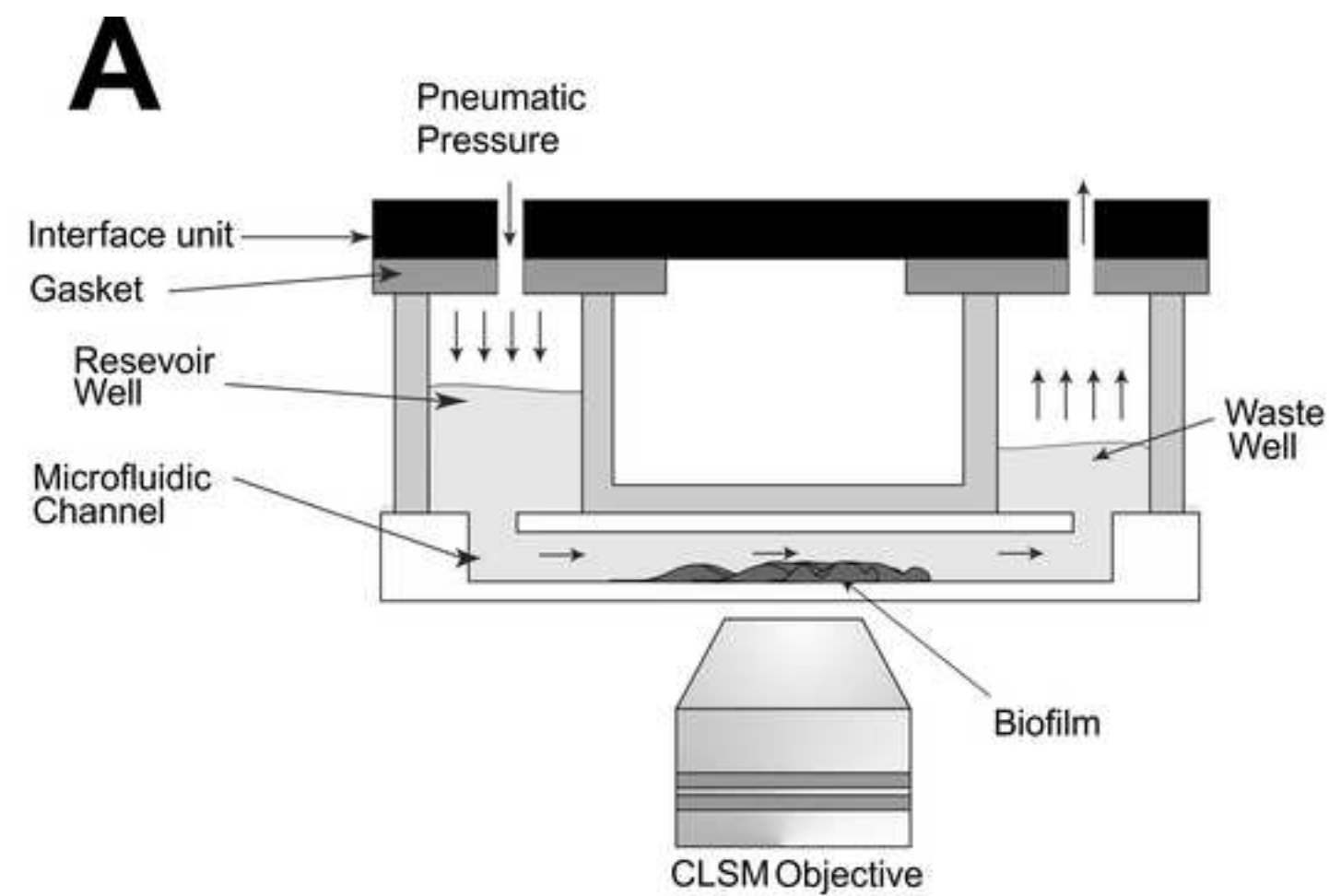


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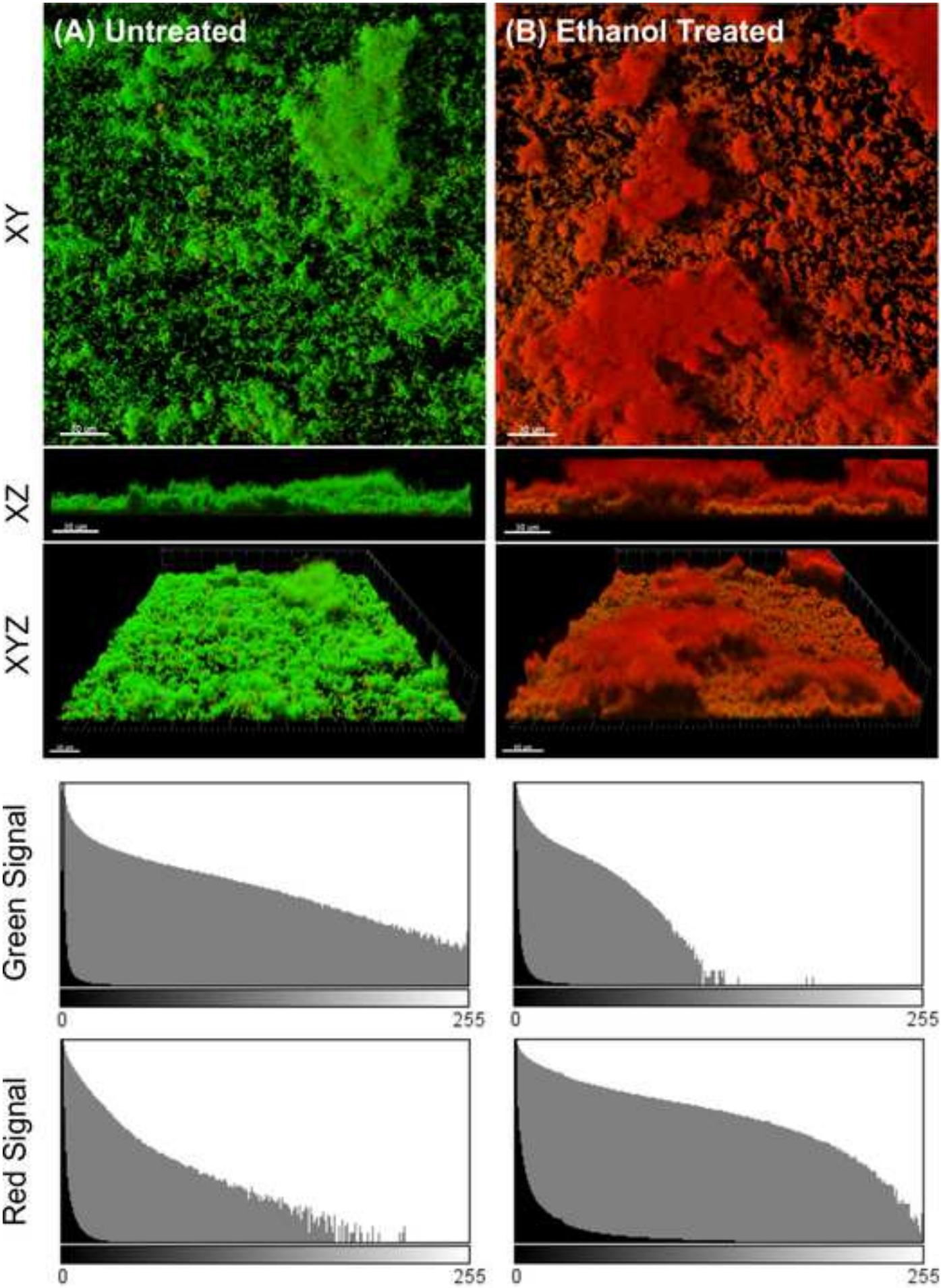
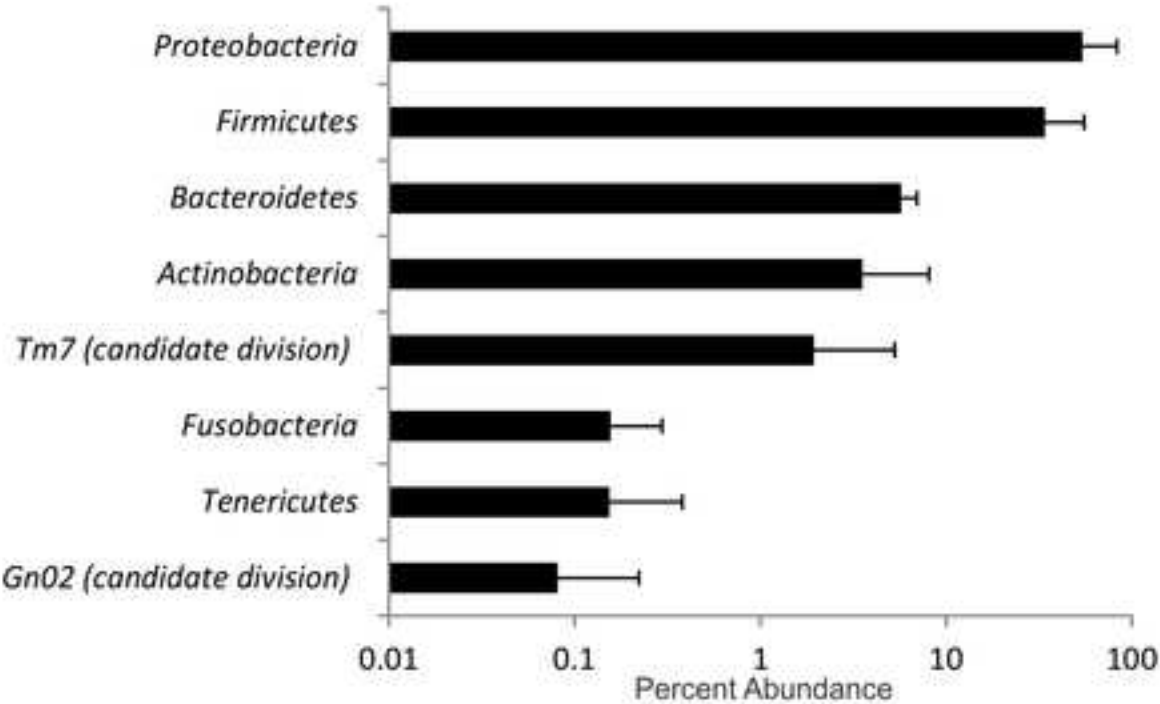
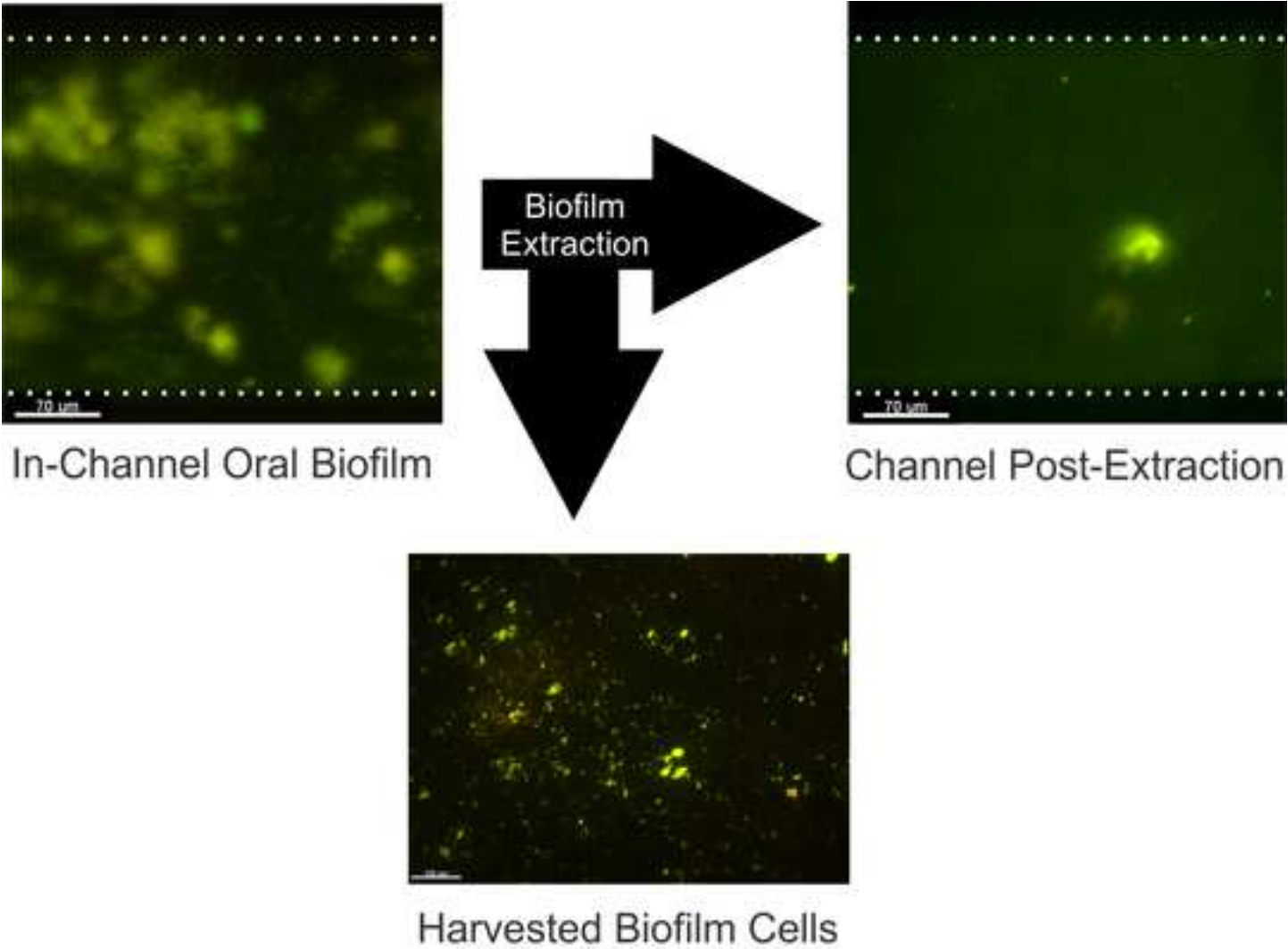


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Community Analysis by 454 Pyrosequencing

Table 1. Quantification of biofilm properties of untreated and 70% ethanol treated :

Parameter/Treatment	Untreated
Average Viability (%)	80.8 (0.9)
Average Biovolume ($\mu\text{m}^3/\mu\text{m}^2$)	17.7 (8.4)
Average Thickness (μm^2)	23.3 (11.3)
Average Roughness	0.4 (0.3)

22 h biofilms developed in pooled cell-free saliva (CFS) from an inoculum cell-containing saliva (CCS). Bold

70% EtOH
28.3 (5.8)**
16.1 (3.0)
15.6 (6.4)
0.50 (0.2)

I values are the averages and non-bolded values in brackets are the standard deviations). Data is from at

≥least five images from three microfluidic channels. Significant differences to the untreated control are

highlighted by an asterisk (*: $P < 0.05\%$; ** $P < 0.01\%$).

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Falcon 50mL Conical Centrifuge Tubes
Falcon 15mL Conical Centrifuge Tubes
Dithiothreitol (White Crystals or Powder/Electrophoresis), Fisher BioReagents
Sorval ultracentrifuge (SS-34 compatible)
Thermo Scientific SS-34 Rotor
Thermo Scientific Type 1 Reagent Grade Deionized Water
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Glycerol
BioFlux microfluidic system
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LIVE/DEAD stain (Invitrogen)
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Thermo Fisher Scientific Inc	NC0542269
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Multiple choices	Multiple choices
Fisher Scientific	04-355-122
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7. Please describe centrifuge speeds as "x g" instead of "g" or the machine-dependent "rpm". For instance in step 1, substep 4.

Thanks for spotting this error – corrected to "x g".

8. Please re-write steps of your protocol section in imperative tense, as if you are telling someone how to do the technique (i.e. "Do this", "Measure that" etc.). for instance, In step 1, substep 2, the

sentence should read “ Collect saliva in a 50 mL...”, Also see step 2, sub step 5. Etc. Please ensure that the entire protocol is written in imperative tense.

Corrected throughout.

9. Please simplify steps of your protocol section so that individual steps contain only 2-3 actions per step. For example, see step 3. Please apply this throughout the protocol section.

Done.

10. Written paragraph below step 4 is not numbered. Please make sure that all the highlighted steps are filmable action items. If not please, un-highlight. Please incorporate this into the protocol step, or as a note.

Done.

11. For the image analysis section please provide screen shot captures of the software used. For filming please see additional information in the scriptwriter file for successful scripting and filming.

We tried to do this but the screen shot images are not particularly informative. This is in part because the part for filming is on the Leica system. The use of IMARIS and COMSTAT is not for filming because we know that many other groups use different types of software. For this reason we suggest stopping at the image collection point but can show in the storyboard how an OME is created for exchange between different software programs.

12. Please revise the protocol text to avoid the use of any pronouns (i.e. "we", "you", "your", "our" etc.). If you feel it is very important to give a personal example, you may use the royal "we" sparingly and only as a "NOTE:" after the relevant protocol step. Please use the Ctrl+F function to find and replace the pronouns.

Done.

13. After you have made all of the recommended changes to your protocol (listed above), please re-evaluate the length of your protocol section. There is no page limit for the protocol text, but there is a 3 pages limit for filmable content. If your protocol is longer than 3 pages, please highlight (in yellow) 2.75 pages (or less) of text to identify which portions of the protocol are most important to include in the video; i.e. which steps should be visualized to tell the most cohesive story of your protocol steps. Please see JoVEs instructions for authors for more clarification. Remember that the non-highlighted protocol steps will remain in the manuscript and therefore will still be available to the reader.

Done.

14. The editor removed the embedded figures from the manuscript. Figure legends, are retained within the manuscript text, directly below the Representative Results text.

Okay. The figures are still in my version that I downloaded. Feel free to remove.

15. Ensure that each figure or data table must have an accompanying legend including a short title,

followed by a short description of each panel and/or a general description. All figures showing data must include measurement definitions and error bars (if applicable).

Done.

16. In some images you mention that they are reproduced with permission. Please provide the copyright permission for JoVE's recordkeeping.

Included with submission.

17. Please make sure to define scale and the units in the figure legends for respective figures.

Done.

18. Please include all the tables separately in editorial manager as an Excel file.

Done. Included as embedded table in Word file and Excel. Please feel free to remove one or other at your discretion.

19. Please make sure that the "Discussion" section covers the following points running between 3 – 6 paragraphs.

a. Critical steps within the protocol.

b. Modifications and troubleshooting.

c. Limitations of the technique.

d. Significance of the technique with respect to existing/alternative methods.

e. Future applications or directions after mastering this technique.

Slight changes in the Discussion have been made. We think that each of these elements are touched upon and also addressed the limitations of this (and any) biofilm model system.

20. Please make sure that your references comply with JoVE instructions for authors. In-text formatting: corresponding reference numbers should appear as superscripts after the appropriate statement(s) in the text of the manuscript. Citation formatting should appear as follows: (For 6 authors or less list all authors. For more than 6 authors, list only the first author then *et al.*): [Lastname, F.I., LastName, F.I., LastName, F.I. Article Title. *Source*. Volume (Issue), FirstPage – LastPage, doi:DOI, (YEAR).]

We used Endnote to generate the reference list. We have amended the reference list as best as we can to be in-line with the formatting. We think it now complies – in particular we noticed that the volume listing was not in bold, the year was in the wrong place, and author initials did not have periods after the initials. We noticed that DOI was not available with some papers via Endnote (see Smith, 1964 and Anon., CDC paper).

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