

Bacterial Community Change during Biofilm Development in the Arctic Marine Environment

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ABSTRACT

Biofilm is an important life form of microorganisms formed in aquatic environments including oral cavities, water supply systems, fresh water and marine environments. They affect human health and water quality. It also has important ecological roles in aquatic environments such as protection from environmental stress and efficient lysis of macromolecules. In this study, we analyzed bacterial community change during biofilm development in coastal area of Svalbard, Norway. High throughput sequencing technology was applied to determine bacterial community structures of biofilm samples collected once a day for 15 days. The major phyla were *Bacteroidetes* (45.4%), *Alphaproteobacteria* (38.6%), and *Gammaproteobacteria* (8.9%). Thirty two major OTUs (>2%) clustered by 97% sequence similarity cutoff mostly belonged to *Rhodobacterales* (26.5%) of *Alphaproteobacteria* and *Flavobacteriales* (15.2%) of *Bacteroidetes*. The major OTUs occupied approximately 45% of the whole community. They were assigned to the genera *Arenicella*, *Flavivirga*, *Hoeflea*, *Litoreibacter*, *Maribacter*, *Octabecabacter*, *Pelagibacter*, *Planktomarina*, *Planktotlea*, *Polaribacter*, *Reseovarius*, *Ruthia*, *Sulfitobacter*, *Tenacibaculum* and several candidatus genera. Some of them were major components in the early phase and the others were major in the late phase.

SAMPLING

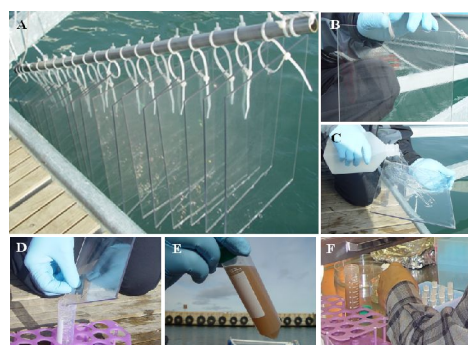
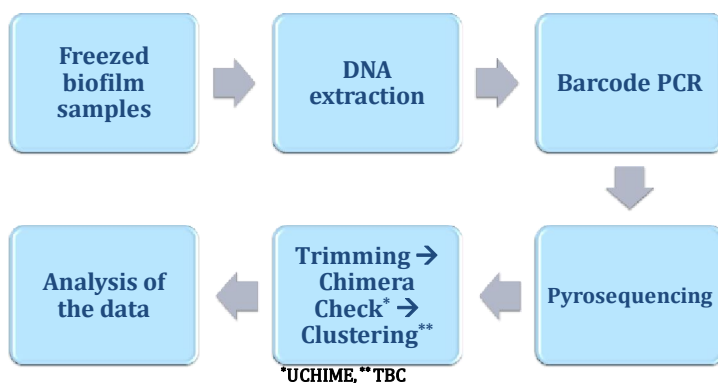


Fig.1. Biofilm formation and sampling procedure. **A**, Polycarbonate acryl plates were submerged in the sea water; **B**, biofilm on acryl plates; **C**, rinsed with sterilized sea water; **D**, scraped the biofilm; **E**, collected samples; **F**, preserved with glycerol for cultivation or frozen for DNA extraction.

STUDY SCHEME



COMMUNITY CHANGE

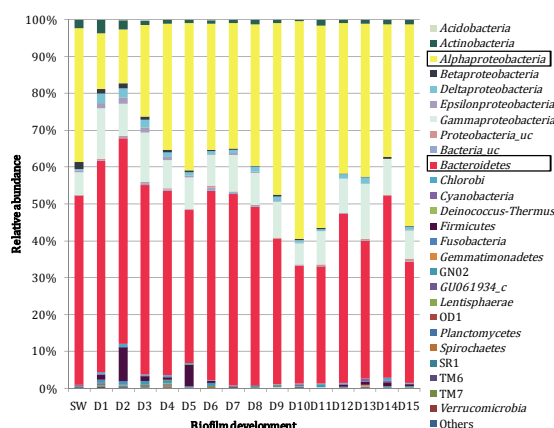


Fig. 2. Relative abundance of phyla or class in the Arctic marine biofilm for 15 days

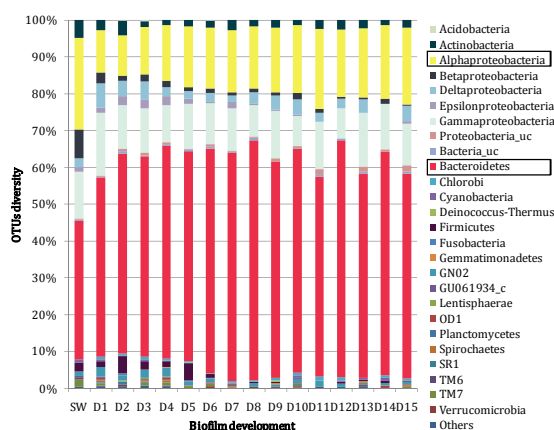


Fig. 3. OTUs diversity of phyla or class in the Arctic marine biofilm for 15 days

HEAT PLOT of RELATIVE ABUNDANCE of MAJOR OTUs

OTU_ID	Taxa	D1	D2	D3	D4	D5	D6	D7	D8	D9	D10	D11	D12	D13	D14	D15
OTU_5	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>Polaribacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_10	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>Flavivirga</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_12	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>EF016484_g</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_13	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>Polaribacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_27	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>ABVV_g</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_38	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>DQ090883_g</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_52	<i>Gammaproteobacteria</i> , <i>Ruthia</i> , <i>o_Ruthia</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_55	<i>Alphaproteobacteria</i> , <i>SAR11</i> , <i>Pelagibacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_57	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>ABVV_g</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_85	<i>Alphaproteobacteria</i> , <i>EH491744_o</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_87	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Planktomarina</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_9	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Sulfitobacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_11	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Litoreibacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_14	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>Flavobacteriaceae_uc</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_17	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>DQ906732_g</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_21	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Sulfitobacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_22	<i>Gammaproteobacteria</i> , <i>Arenicella</i> , <i>o_Arenicella</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_29	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Sulfitobacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_35	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>Tenacibaculum</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_36	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>Flavobacteriaceae_uc</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_39	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>DQ395037_g</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_42	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>Maribacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_83	<i>Bacteroidetes</i> , <i>Flavobacteriales</i> , <i>Flavobacteriaceae_uc</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_169	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Planktotlea</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_1	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Sulfitobacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_2	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Planktotlea</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_3	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Sulfitobacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_4	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Octadecabacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_7	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Hoeflea</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_8	<i>Alphaproteobacteria</i> , <i>Rhodobacterales</i> , <i>Reseovarius</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_16	<i>Bacteroidetes</i> , <i>Sphingobacteriales</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTU_18	<i>Gammaproteobacteria</i> , <i>Arenicella</i> , <i>o_Arenicella</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Fig.4. Change of relative abundance in Major OTUs ($\geq 2\%$)

DNA CONTENTS CHANGE of MAJOR OTUs

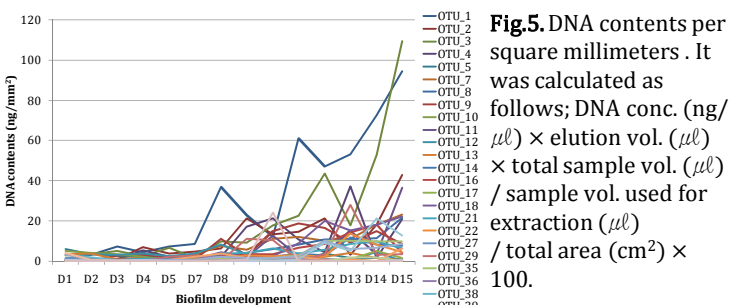


Fig.5. DNA contents per square millimeters. It was calculated as follows; DNA conc. (ng/ μ l) \times elution vol. (μ l) \times total sample vol. (μ l) / sample vol. used for extraction (μ l) / total area (cm²) \times 100.