OFFSHORE PRODUTION: EXPIRIENCE IN ADVANCED DIAGNOSIS OF MICROBIAL CONTAMINATION

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ABSTRACT

A diferencia de las actividades de exploración y producción convencional en tierra, donde básicamente en todos los campos hay reúso y reinyección de agua, la exploración cuesta afuera puede ser hecha sin el reúso del agua producida, utilizando solamente agua del mar para inyección. Independiente del modo de operación (con o sin reúso), el cuidado microbiológico es importante para evitar problemas relacionados a la presencia y desarrollo de microorganismos, como MIC (corrosión influenciada por microorganismos), biofouling y generación de H2S.

Una herramienta importante para conocer los puntos críticos de contaminación microbiana en una FPSO (en inglés Floating, Production, Storage and Offloading) y mejorar el régimen de adición de biocidas son los relevamientos microbiológicos avanzados. De esta manera se puede seleccionar el tratamiento adecuado en términos de que biocida utilizar, donde dosificar, en que concentración y con qué frecuencia.

En ese trabajo vamos a presentar dos relevamientos de casos de estudio reales: Uno realizado en 6 FPSOs distintas en Brasil, evidenciado que mismas unidades próximas pueden tener perfiles distintos cuanto al nivel de contaminación. El segundo, una FPSO con reúso y reinyección de agua, demostrando la importancia del tratamiento del agua producida.

INTRODUCTION

Offshore exploration of oil and gas is becoming more relevant around the world. In Brazil, for example, 90% of the total oil came from offshore fields (Petrobras strategic plan). FPSOs (Floating Producing Storage and Offloading) are the most common vessels used for this operation since they are less expensive, more flexible and efficient, and safer, compared to traditional offshore oil and gas platforms. A typical layout for seawater treatment on FPSOs includes seawater intake hoses/boxes, lift pumps, filters, deaerators, guard filters and high-pressure feeding pumps for nanofiltration membranes (NF), heat exchangers, water injection pumps and manifolds. Fresh sea water is the main source of water injection. The reinjection of produced water is still not standard

for most offshore units, however, there is an increase in interest to reinjected produced water and special attention is needed regarding microbiological treatment of these waters.

Usually, units that inject fresh seawater have a Sulfate Removing Plant (SRP) that utilize nanofiltration (NF) membranes to selectively remove sulfate and other divalent ions from the water to minimize risk of scaling. Deaerator towers can be installed upstream or downstream of the SRP depending on the project and are very important to avoid corrosion by oxygen in injection systems. SRP performance is affected by biofouling if the chemical treatment and pre-treatment are not optimized, what can also contribute to Microbially Induced Corrosion (MIC) of injection lines. To mitigate these problems, the common chemical treatments used in Brazilian FPSOs consist of electro-chlorination, scale inhibitors, oxygen scavengers and organic biocides.

In some offshore units, besides fresh sea water injection, there is also reinjection of produced water for secondary recovery operations. This combination of water streams requires an extended water management program. Therefore, these waters undergo treatments that vary and are often region or system specific. A rigorous microbial control program is required to avoid issues caused by microorganisms such as microbial influenced corrosion, biofilm formation, H2S production by sulfate-reducing bacteria (SRB) and reduced oil and gas quality.

Some key process parameters (temperature, flow rate, oxygen levels) and changes to the chemical treatments can lead to important variations on the microbial communities what can impact performance of topside equipment (Van der Kraan *et al.* 2018). In this work, two cases studies highlighting the importance of a good monitoring of microbial contamination and selection of an appropriate treatment are presented The first studies purpose was to investigate microbial contamination quantitatively and qualitatively, using advanced molecular biology techniques, and describe the dominant microbial communities found in each stage of the water treatment systems for six FPSOs that only had injection of fresh seawater.

The second study will present results suggesting that careful routine monitoring of FPSO systems is needed and the addition of a sustainable microbial control active is strongly suggested in order to control microbial populations and extend the lifespan of equipment and infrastructure.

FIRST CASE

Experimental part

The six FPSOs selected for this study produce from 16,000 to 24,000 m^3/day of treated water. FPSOs A, B and C have a deaerator upstream of the NF membranes while FPSOs D, E and F have the deaerator located downstream of the membranes. FPSOs A, B, C and D are located about 300 km from the Brazilian coast in a common radius of 30 km. FPSOs E and F are located about 500 km to the north of A, B, C, D and 80 km from the coast, at 15 km distance.

Advanced diagnostics of microbial contamination

Representative water samples were collected in duplicate from the different stages of the treatment process for each FPSO (A, B, C, D, E, F). The DNA of selected water samples were extracted (Mo-Bio extraction kit) and analyzed using molecular biology techniques including:

Total Cell determination using quantitative Polymerase Chain Reaction (qPCR). The total cell numbers were determined using the 16S rDNA gene. According to Klappenbach *et al.* (2001) the average appearance of this gene per bacterial cell is estimated to be between 2 and 4 copies per genome whereas for archaeal cells, copy numbers are between 1 and 2 copies per genome (Dar *et al.* 2007). Two primer sets were used to determine cellular numbers in the system. Primer set 1 and primer set 2 were prepared using published methods by Gittel *et al.* (2009). For Sulfate Reducing Microbes (SRM) determination, one primer pair was used to target a subunit of a protein involved in the sulfate reduction pathway. This dissimilatory sulfate reduction gene (DSR) is shared amongst all sulfate-reducing microorganisms. The primer sets published by Foti *et al.* (2007) and Dar *et al.* (2007) were used.

Next Generation Sequencing (NGS) for identifying the dominant classes of microorganisms. Selected samples were chosen for next generation sequencing using Illumina MiSeq v3 reagent kits. The read length is 2×300 base pairs. Results were analyzed using the open source software platform MOTHUR and QIIME .

Results and Discussion

FPSO A was the vessel that presented the highest microbial loads from intake to injection. Figure 1 shows a simplified diagram of seawater treatment on FPSO A and the respective microbial condition of each sampling point (triangles) related to total bacterial cells. qPCR results (Figure 2) show a growth trend throughout the water flow, clearly demonstrating that the biocide treatment with THPS (tetrakis(-hydroxymethyl- phosphonium sulfate) and DBNPA (2,2-Dibromo-3-nitrilopropionamide) was ineffectual. THPS was dosed downstream to NF membranes in (2 times per week batches at 150 ppm active) and DBNPA upstream to membranes, also in batches (2 times per week batches at 40 ppm active).

NGS results identified Gammaproteobacteria as the main class found in all sampling points (present at 78%-100% relative population distribution). The genus Pseudoalteromonas was dominant (30%-70%) in all sampling points, except the basket filters where Acinetobacter was dominant (57%) and the guard filter where Alteromonas was dominant (42%). The genus Vibrio was also found (10%) in the SRP feed water. A common problem observed for FPSOs A, B and C is the unexpected, localized corrosion of metallic coupons installed in anoxic zones downstream of the SRP system. A possible explanation is the fact the Pseudoalteromonas sp. has been described

as a key contributor to the MIC process of seawater systems containing carbon or stainless steel (Moradi *et al.* 2021; Li *et al.* 2016).

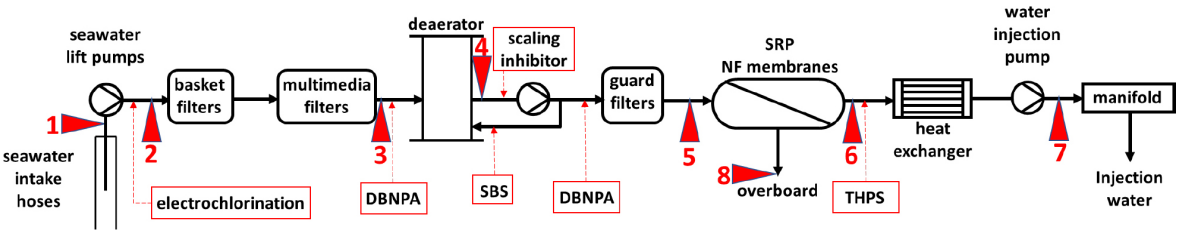

Figure 1. Simplified flow diagram of seawater treatment for FPSO A. Triangles indicates sampling points and its color indicates the level of total bacterial cells/mL (red: > 104; yellow: ~ 103; green < 102; colorless: not sampled).

FPSO A	Total Bacteria	SRM	Dominant Genera
1 - Seawater Intake	10^4	10^1	*76% Pseudoalteromonas* *10% Alteromonas* *5% Acinetobacter*
2 - Basket Filters	10^5	10^2	*14% Pseudoalteromonas* *57% Acinetobacter*
3 - Multimedia Filters	10^5	10^2	*92% Pseudoalteromonas* *1% Alteromonas* *1% Acinetobacter*
4 - Deaerator	10^5	10^2	*78% Pseudoalteromonas* *11% Alteromonas* *1% Acinetobacter*
5- -SRP Inlet	10^4	10^2	*29% Pseudoalteromonas* *42% Alteromonas* *8% Vibrio* *1% Acinetobacter*
6 - SRP Permeate	10^5	10^1	*90% Pseudoalteromonas* *2% Acinetobacter*
7 - Injection Water	10^5	10^2	*89% Pseudoalteromonas* *2% Acinetobacter* *3% Pseudomonas*
8 - SRP Reject	10^6	10^2	*84% Pseudoalteromonas* *4% Alteromonas* *5% Thalassospira* *1% Pseudomonas*

Figure 2. Relative bacterial genera distribution and cell quantification (total, SRM) for selected samples on FPSO A.

FPSO B is a similar system to FPSO A, with the deaerator upstream of the SRP. The system uses electrochlorination after the intake hoses and there was a low microbial load observed (≤ 102 cells/mL) for most sampling points (Figure 3).

Due to the low bacterial contamination, NGS analyses were only possible for 2 sampling points (Dearetor and SRP Inlet) with the highest contamination levels. Alteromonas (83%) and

Pseudoalteromonas (11%) were the dominant genera after the deaerator. A wide variety of organisms were found in the SRP feed water (point 5) and the dominant class was Alphaproteobacteria (43%) followed by Gammaproteobacteria (22%). The main genus found was Cohaesibacter (8%), a known nitrate reducer.

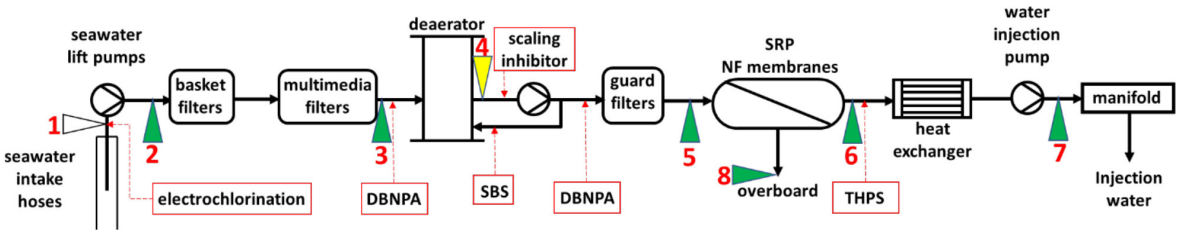

Figure 3. Simplified flow diagram of seawater treatment for FPSO B. Triangles indicates sampling points and its color indicates the level of total bacterial cells/mL (red: > 104; yellow: ~ 103; green < 102; colorless: not sampled).

FPSO B	Total Bacteria	SRM	Dominant Genera
1 - Seawater Intake	< 10	< 10	Not Avaiable
2 - Basket Filters	10^2	10^1	Not Avaiable
3 - Multimedia Filters	10^1	< 10	Not Avaiable
4 - Deaerator	10^3	< 10	*83% Alteromonas* *11% Pseudoalteromona*
5- -SRP Inlet	10^2	10^1	*8% Cohaesibacter* *5% Paracoccus* *1% Nesiotobacter* *1% Nautella* *4% Neptunomonas*
6 - SRP Permeate	< 10	< 10	Not Avaiable
7 - Injection Water	10^1	< 10	Not Avaiable
8 - SRP Reject	10^1	< 10	Not Avaiable

Figure 4. Relative bacterial genera distribution and cell quantification (total, SRM) for selected samples on FPSO B.

FPSO C has a similar chlorination system as in FPSO B and low microbial load (≤102 cells/mL) was also observed for most sampling points (Figures 5 and 6). Despite the similar layout and proximity to FPSOs A and B, FPSO C presented a different microbial population.

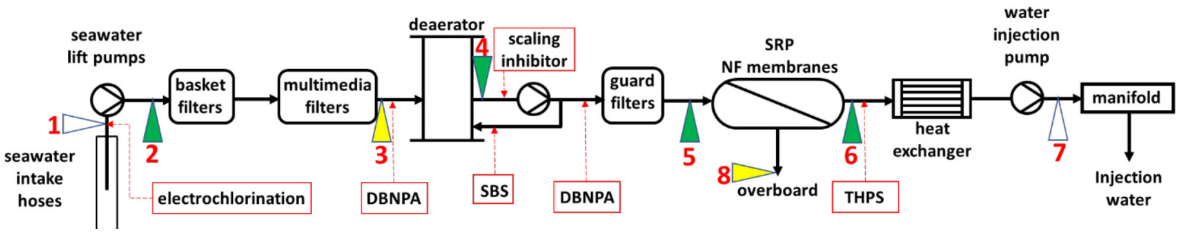

Figure 5. Simplified flow diagram of seawater treatment for FPSO C. Triangles indicates sampling points and its color indicates the level of total bacterial cells/mL (red: > 104; yellow: ~ 103; green < 102; colorless: not sampled).

FPSO C	Total Bacteria	SRM	Dominant Genera
1 - Seawater Intake	< 10	< 10	Not Avaiable
2 - Basket Filters	10^2	10^1	Majority unclassified *3% Sphingomonas* *9% Deinococcus*
3 - Multimedia Filters	10^3	10^1	Majority unclassified *10% Anderseniella* *1% Vibrio* *1% Rhodopirellula*
4 - Deaerator	10^2	< 10	Not Avaiable
5- -SRP Inlet	10^2	10^1	*71% Cohaesibacter* *4% Ruegeria* *2% Labrenzia* *1% Filomicrobium* *1% Waddlia* *1% Cutibacterium*
6 - SRP Permeate	10^1	10^1	Not Avaiable
7 - Injection Water	10^1	< 10	Not Avaiable
8 - SRP Reject	10^3	10^1	*54% Thiomicrospiraceae* *6% Hydrogenovibrio* *1% Rhodobacteraceae* *1% Ruegeria*

Figure 6. Relative bacterial genera distribution and cell quantification (total, SRM) for selected samples on FPSO C.

As shown in Figure 7, FPSO D presented microbial load increases within the system from ~10^2 cells/mL to 10^3 cells/mL for the SRP feed water. Counts were reduced to low levels in the SRP permeate but then increased on the way to the injection header to 1.2x10^3 cells/mL. There is an opportunity to improve the biocide treatment. Alphaproteobacteria dominates (50%-88%), especially in the injection water within the genus Ruegeria (35%).

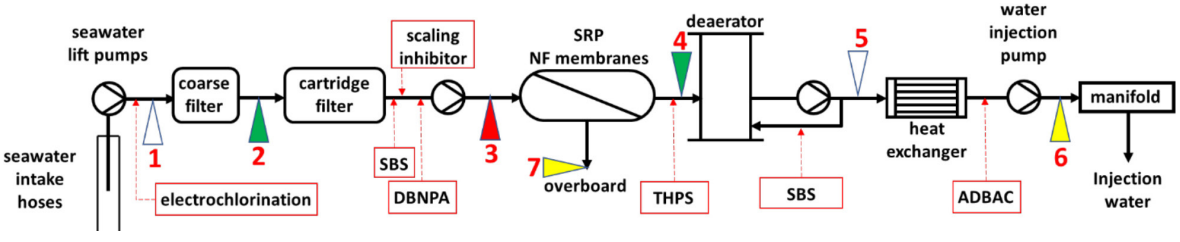

Figure 7. Simplified flow diagram of seawater treatment for FPSO D. Triangles indicates sampling points and its color indicates the level of total bacterial cells/mL (red: > 10^4; yellow: ~ 10^3; green < 102; colorless: not sampled)

FPSO D	Total Bacteria	SRM	Dominant Genera
1 - Seawater Intake	< 10	< 10	Not Avaiable
2 - Corse Filters	10^2	10^1	Not Avaiable
3 - SRP Inlet	10^3	< 10	Majority of genus unclassied *19% Thiomicrospiraceae unclassified* *3% Hydrogenovibrio* *2% Rhodobacteraceae_unclassified* *1% Rhodopirellula*
4 - SRP Permeate	10^1	10^2	Not Avaiable
5 - Deaerator	< 10	< 10	Not Avaiable
6 - Injection Water	10^1	10^1	*35% Ruegeria* *20% Rhodobacteraceae_unclassified* *12% Cribrihabitans* *8% Alphaproteobacteria_unclassified*
7 - SRP Reject	10^2	10^1	*54% Thiomicrospiraceae unclassified* *6% Hydrogenovibrio* *1% Rhodobacteraceae_unclassified* *1% Ruegeria*

Figure 8. Relative bacterial genera distribution and cell quantification (total, SRM) for selected samples on FPSO D.

In FPSO E, microbial contamination was relatively controlled (~ 10^2 cells/mL) upstream of the membranes but increased in the deaerator up to 10^4 cells/mL This sampling point was immediately downstream of THPS treatment (2 times per week batches at 150 ppm active), indicating this biocide was clearly ineffectual. Alphaproteobacteria (Magnetospira, 36-39%) dominated the points upstream of the membranes while Gammaproteobacteria dominated the locations downstream of the membranes, mainly by Alcanivorax (21-30%), a known genus typical of hydrocarbon degraders (McGenity *et al.*, 2012).

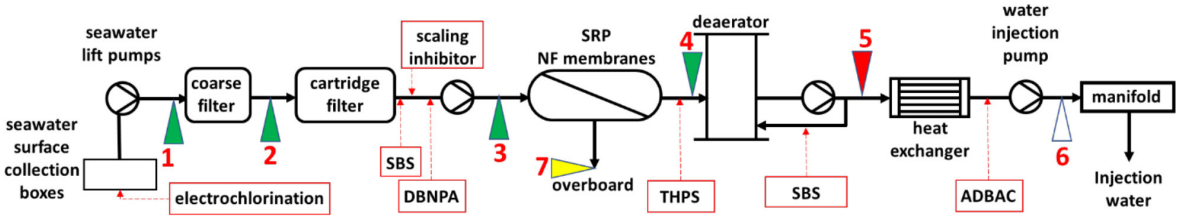

Figure 9. Simplified flow diagram of seawater treatment for FPSO E. Triangles indicates sampling points and its color indicates the level of total bacterial cells/mL (red: > 10^4; yellow: ~ 10^3; green < 10^2; colorless: not sampled).

FPSO E	Total Bacteria	SRM	Dominant Genera
1 - Seawater Intake	10^2	10^1	*34% Magnetospira* *10% Alphaproteobacteria unclassified*
2 - Corse Filters	10^3	10^2	*31% Magnetospira* *14% Alphaproteobacteria unclassified*
3 - SRP Inlet	10^2	10^1	Not Avaiable
4 - SRP Permeate	10^1	< 10	*21% Alcanivorax* *1% Pseudoalteromonas* *7% Mycobacterium*
5 - Deaerator	10^4	10^3	*30% Alcanivorax* *6% Marinobacter* *1% Pseudoalteromonas*
6 - Injection Water	< 10	< 10	Not Avaiable
7 - SRP Reject	10^3	10^1	Not Avaiable

Figure 10. Relative bacterial genera distribution and cell quantification (total, SRM) for selected samples on FPSO E.

FPSO F is the system with the best microbial control with just one sampling point reaching 1x103 cells/mL downstream of the DBNPA dosage (2 times per week batches at 40 ppm active) and upstream of the NF. Alphaproteobacteria (Unclassified, 65%) dominates all points. The main identified genera were Magnetospira (22%), a strictly aerobic organism that can live in symbiosis with acid producing bacteria (Araujo *et al.*, 2014).

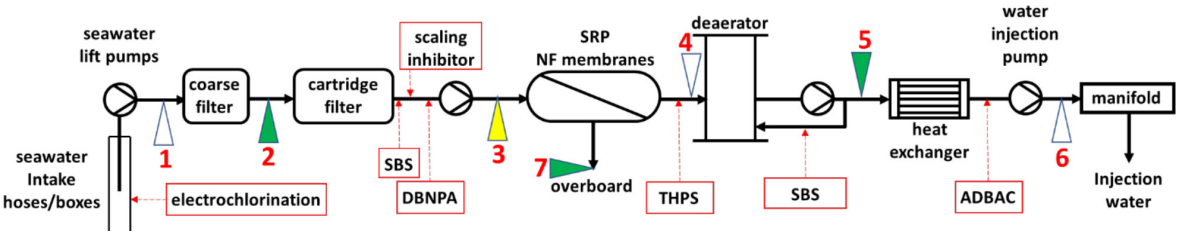

Figure 11. Simplified flow diagram of seawater treatment for FPSO B. Triangles indicates sampling points and its color indicates the level of total bacterial cells/mL (red: > 10^4; yellow: ~ 10^3; green < 10^2; colorless: not sampled).

Final Considerations

The results presented in the FPSO work evidence the importance to have a good microbiological evaluation program and treatment. Similar FPSOs, located within a 30 km radium (A, B, C and D) presented significantly different in term of microbial load and dominant genera.

FPSO A presented the worst condition regarding microbial counts while FPSO F had the best microbial control. In most cases, bacterial regrowth downstream of the chlorination system was evident, indicating excess biofilm formation and reinoculation of the water. This situation was more concerning with FPSOs A, D and E where a high level of contamination can reach the reservoir via the injection water, causing a risk for loss of injectivity/productivity and reservoir contamination/souring.

FPSO F	Total Bacteria	SRM	Dominant Genera
1 - Seawater Intake	< 10	< 10	Not Avaiable
2 - Corse Filters	10^2	10^1	41% Alphaprotebacteria *27% Anderseniella* *19% Magnetospira* *3% Cutibacterium* *1% Thiogranum* *1% Predibacter*
3 - SRP Inlet	10^2	10^1	*65%* a-prot. unclassified *10% Anderseniella* *4% Ruegeria* *2% Predibacter*
4 - SRP Permeate	< 10	< 10	Not Avaiable
5 - Deaerator	10^2	< 10	Not Avaiable
6 - Injection Water	< 10	< 10	Not Avaiable
7 - SRP Reject	10^2	< 10	59% Alphaproteobacteria *9% Ruegeria* *1% Cutibacterium* *3% Bdellovibrio* *3% Bythopirellula*

Figure 12. Relative bacterial genera distribution and cell quantification (total, SRM) for selected samples on FPSO F.

Upstream of the membranes, the use of less complex glycols in the 20% DBNPA formulation apparently stimulated bacterial regrowth when the biocide active disappears while downstream of the nanofiltration membranes, there was a clear need to improve microbial control since the incumbent THPS/ADBAC treatment was not performing adequately. As next step, we recommend evaluate other biocides, like glutaraldehyde, especially downstream of the sulfate removal membranes, since in contrast to THPS, it will not add sulfates back to the injection water, and by this way avoid the risk of stimulating sulfate reducing organisms on the reservoir.

SECOND CASE

System Description

Produced hydrocarbons and water are sent to the separator, from multiple wells, where the oil and gas is separated from the water. This water contains variable levels of H_2S and is subsequently pumped to a turret. Simultaneously, seawater is taken in from the ocean and pumped through a deaerator tower, where the water is chlorinated and stripped of oxygen using N_2 uplifting. The effluent from the deaerator is amended with nitrate and pumped to the same turret. Here, it is mixed with the water from the separators and injected back into the subsurface using subsea injectors. The average temperature of the wells is around 60 ˚C.

Experimental part

Water collection, DNA extraction, and qPCR (for subgroup quantification) and NGS (to identify dominant classes of microorganisms) were performed using the same method described in case 1.

Results

Data from qPCR analysis is presented in Figure 13.

Seawater intake - Relatively low contamination. Pseudomonas sp. as the most common genera. There was no detection of Archea or SRM in the system.

Deaerator - High contamination rate with a wide microbial diversity, able to exhibit a range of different metabolic activities. About 50-65% of the species can be assigned to various Methylophaga species, which are known for the oxidation of methane or methanol and are commonly found in brackish marine waters. The N2 addition causes oxygen to diminish, making this the starting point for detrimental metabolic processes such as sulfide generation, which may lead to microbial induced corrosion. Results demonstrated that approximately 104 cells mL-1 of SRM were present at this location. Nitrate addition just after the deaerator provides a starting point for denitrification (nitrate reduction) later in the system. Most Archaeal sequences were assigned to the genus Nitrosopumilus, a common seawater dwelling Crenarchaeota that can oxidize ammonia to nitrite.

Turrets - High level of contamination at the turrets where the sea water (daeerated and with nitrate addition) is mixed with water from the separators. The dominant groups belong to the Epsilonproteobacteria family, which displays a variety of sulfur and sulfide oxidation processes under either oxygenic or denitrifying conditions. Over 50% of the sequences were classified as Thiomicrospira, which are sulfur and sulfide oxidizers. Nitrate-reducing microorganisms are heavily enriched at this site due to nitrate addition downstream of the deaerator. This indicates that nitrate addition has a strong selective influence on the community.

Separators - High bacterial counts were observed. Between 70% and 90% of detected the bacteria were SRM (Desulfocaldus-like species). As water passes through a separator, the SRM community is mixed with a community of fermenting microorganisms. The communities differ within each of the sampled waters, although diversity analyses suggest that the SRM composition is relatively constant among the different wells.

	Total Bacteria (cell/mL)	Total Archea (cell/mL)	Total SRM (cell/mL)	Toal NRP (cell/mL)
Seawater Intake	10^2	< 10	< 10	10^1
Deaerator Effluent	10^6	10^3	10^1	10^4
Turret (Produced/seawater)	10^6	10^{3-4}	10^5	10^5
Water Separator	10^{4-5}	10^{2-3}	10^{4-5}	10^2

Figure 13. Cell quantification (total Bacteria, total Archea, total SRM and total nitrate-reducing prokaryotes (NRP)).

Final Considerations

Separators contained high numbers of SRM, composing up to 90% of the total population, and were accompanied by likely thermophilic, fermentative species. Deaerator represents a high concern for this system. Microbial cell numbers were increased 5 orders-of-magnitude compared to seawater, and likely indicate that these components act as large-scale incubators the effluent water. Species identified in the deaerator comprise a diverse microbial community with varied metabolic lifestyles. Nitrogen (N2) uplift in the deaeration towers, used to strip oxygen, facilitates anaerobic metabolism and encourages detrimental processes such as sulfate-reduction and iron-reduction that may lead to microbial induced corrosion.

Deaerated, nitrate-rich water is combined with sulfide-rich water from the oil-water separators at the subsea injection turrets. The continuous association and mixing of chlorinated seawater, H2S-rich production water, and nitrate-amended seawater selectively gave rise to populations of microorganisms that may be able to oxidize sulfur compounds under nitrate-reducing conditions and reduce hydrogen sulfide levels, but the high cell numbers encouraged by the nitrate additions may also stimulate biofouling.

This microbial audit indicates that chlorination and nitrate-treatment alone may not substantially reduce the number of microorganisms present in FPSO production facilities. However, further investigation would be needed to understand the efficacy of different treatment programs.

CONCLUSIONS

Similar to what is done on onshore sites, microbial evaluations are an important tool for offshore production units. The use of molecular biology techniques allows for a better understanding of the microbial population, metabolic dynamics and helps in the identification of hotspots in early stages. Even in FPSO units that are not very distant from each other and that use only fresh sea water for injection, it is possible to see huge differences regarding microbial contamination in both total microbial contamination and dominant genera of bacteria. Early identification helps in the microbial control strategy allowing a more efficient, sustainable, and

economical biocide treatment. In systems that also use produced water for re-injection, the water mixture creates a more complex water cycle management and increase the importance of a good microbial monitoring, since produced water usually came with contamination from reservoir, that, if is not properly treated can spread contamination throughout the system.

Microbial monitoring is a very useful tool to evaluate the incumbent biocide treatment. In the two presented cases, it was possible to see that current treatment was not being effective to control the microbial contamination increasing the risk of MIC and souring. Next step for both systems would be to perform a optimization test to evaluate other biocides.

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